

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:43:04 ; Search time 147.538 Seconds  
(without alignment)  
375.236 Million cell updates/sec

Title: US-09-920-137f-7  
Perfect score: 668  
Sequence: 1 QVQLVSGGGVQVQPSURL.....NYTYGMDVWGQITVTIVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657.5	98.4	146	5 AAM51171	Aam51171 Human rec
2	652.5	97.7	146	5 AAM51170	Aam51170 Human rec
3	627.5	93.9	146	5 AAM51169	Aam51169 Human rec
4	620.5	92.9	146	5 AAM51172	Aam51172 Human rec
5	615.5	92.1	146	5 AAM51168	Aam51168 Human rec
6	583	87.3	135	7 ADD28320	Add28320 Human het
7	583	87.3	135	7 ADD28236	Add28236 Human het
8	583	87.3	135	5 ADV86823	Adv86823 Bacillus
9	582	87.1	124	6 ADA89238	Ada89238 Human ant
10	581.5	87.1	127	2 AAY17954	Aay17954 Human D4.
11	581.5	87.1	138	2 AAW80815	Aaw80815 Amino aci
12	581.5	87.1	457	9 AEC16143	Aec16143 Human ant
13	581.5	87.1	523	3 AAY44994	Aay44994 HD70scfv-
14	581.5	87.1	524	3 AAY44995	Aay44995 HD70scfv-
15	581	87.0	126	7 ADK18593	Adk18593 Anti-huma
16	581	87.0	126	7 ADK18785	Adk18785 Anti-huma
17	581	87.0	126	7 ADK18858	Adk18858 Anti-huma
18	581	87.0	126	8 ADL25404	Adl25404 Human mAb
19	579	86.7	126	7 ADK18786	Adk18786 Anti-huma
20	579	86.7	126	7 ADK18822	Adk18822 Anti-huma
21	579	86.7	126	7 ADK18882	Adk18882 Anti-huma
22	579	86.7	126	7 ADK18601	Adk18601 Anti-huma
23	579	86.7	126	8 ADL25420	Adl25420 Human mAb
24	579	86.7	126	8 ADP22222	Adp22222 Human ant

25	577.5	86.5	125	8 ADP22316	Adp22316 Human ant
26	577	86.4	115	5 AAM51164	Aam51164 Anti-tumo
27	577	86.4	141	9 ADV67314	Adv67314 Amino aci
28	576	86.2	118	5 AAM51167	Aam51167 Human DP-
29	575.5	86.2	125	8 ADP22300	Adp22300 Human ant
30	575.5	86.2	125	8 ADP22312	Adp22312 Human ant
31	573	85.8	134	8 ADP22348	Adp22348 Human ant
32	572.5	85.7	252	5 ABP45720	Abp45720 Human Bly
33	572.5	85.7	252	7 ADG96547	Adg96547 Single ch
34	572.5	85.7	451	3 AAY93734	Aay93734 The heavy
35	572.5	85.7	451	6 AAE35889	Aae35889 Human 11.
36	572	85.6	122	8 ADP22128	Adp22128 Human ant
37	572	85.6	126	7 ADK18821	Adk18821 Anti-huma
38	571.5	85.6	123	8 ADS84372	Ads84372 Human ant
39	571.5	85.6	123	8 ADR68514	Adr68514 Anti-Epo-
40	571	85.5	135	7 ADD28317	Add28317 Human het
41	570.5	85.4	125	7 ADE28451	Ade28451 Human ant
42	570.5	85.4	127	9 AEB27731	Aeb27731 Prostate
43	570.5	85.4	252	9 AEB27751	Aeb27751 Anti-pros
44	570.5	85.4	470	7 ADE28475	Ade28475 Human ant
45	569.5	85.3	122	9 AEB45960	Aeb45960 Human mon

#### ALIGNMENTS

RESULT 1  
AAM51171  
ID AAM51171 standard; protein; 146 AA.

XX AAM51171;

DT 10-JUN-2002 (first entry)

XX Human recombinant mAb TNV148 (B) heavy chain variable region.

XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
complementarity determining region; antirheumatic; antiarthritic;  
antitumor; antidiabetic; antiallergic; antiinflammatory; antitickling;  
antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;  
antidiabetic; cardiac; antibacterial; virucide; fungicide; antileptotic;  
protease; cytosolic; neuroprotective; antiparkinsonian; neurotropic;  
human; diagnosis; therapy; TNV148; monoclonal antibody; mAb.

OS Homo sapiens.

XX Synthetic.

XX Key	Location/Qualifiers
FT Peptide	1..19
FT	/label= Signal_peptide
FT	/note= "amino acids 1-7 are PCR primer-encoded and may differ from the native sequence"
FT Protein	20..146
FT	/label= Mature_protein
FT Region	31..49
FT	/label= FR1
FT Region	50..54
FT	/label= CDR1
FT Region	55..68
FT	/label= FR2
FT Region	69..85
FT	/label= CDR2
FT Region	86..117
FT	/label= FR3
FT Misc-difference	94
FT	/note= "wild-type Pro substituted by Ser"
FT Region	118..135
FT	/label= CDR3
FT Misc-difference	126
FT	/note= "encoded by A"
FT Region	136..146
FT	/label= J6
XX	

PN WO200212502-A2.  
 XX 14-FEB-2002.  
 XX 07-AUG-2001; 2001WO-US024785.  
 XX 07-AUG-2000; 2000US-0223360P.  
 PR 29-SEP-2000; 2000US-0236826P.  
 PR 01-AUG-2001; 2001US-00920137.  
 XX (CENZ ) CENTOCOR INC.  
 PA  
 XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
 PI WPI; 2002-217194/27.  
 XX N-PSDB; ABL53511.  
 DR  
 XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 PT angina pectoris, myocardial infarction, leprosy.  
 XX  
 PS Example 3; Fig 4; 131pp; English.  
 XX  
 CC The present sequence is that of the heavy chain variable region of anti-  
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
 CC TNV148(B). TNV148(B) was produced by site-directed mutagenesis of TNV148  
 CC (see AAM51170), replacing residue Pro-94 with a germline Ser. TNV148 was  
 CC 1 of 8 human mAbs produced from a GenIV fusion using spleen cells from a  
 CC hybrid mouse containing human variable and constant region antibody  
 CC transgenes that was immunised with human TNF alpha. The human mAbs bound  
 CC immobilised human TNF alpha with high avidity and had a totally human  
 CC IgG1, kappa isotype. They showed relatedness to each other and to the  
 CC human germline DP-46 heavy chain sequence (see AAM51167). The invention  
 CC provides isolated human, primate, rodent, mammalian, chimeric, humanised  
 CC and/or complementarity determining region (CDR)-grafted anti-TNF  
 CC antibodies and variants, as well as anti-TNF antibody compositions,  
 CC encoding or complementary nucleic acids, vectors, host cells,  
 CC compositions, formulations, devices, transgenic animals, transgenic  
 CC plants, and methods of making and using them. The anti-TNF antibody  
 CC comprises at least a portion of an immunoglobulin molecule, especially  
 CC the heavy chain and/or light chain variable regions given in the present  
 CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. They are useful for diagnosing or treating a TNF  
 CC related condition in a cell, tissue, organ or animal (claimed) such as  
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
 CC Creutzfeldt-Jakob disease. TNV148(B) may be especially useful as an  
 CC antiinflammatory  
 XX  
 SQ Sequence 146 AA;  
 Query Match 98.4%; Score 657.5; DB 5; Length 146;  
 Best Local Similarity 99.2%; Pred. No. 7.3e-49;  
 Matches 126; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 1 QVQLVESGGGVQPGKSLRLSRAAGGFISSVAMHWVRQAPGNGLEWFAVMSYDGSNKKY 60  
 20 QVQLVESGGGVQPGKSLRLSRAAGGFISSVAMHWVRQAPGNGLEWFAVMSYDGSNKKY 79  
 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARDRGIAAGN-YYYYGMDVWGQG 119  
 80 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARDRGIAAGNYYYYGMDVWGQG 139

Qy 120 TTVTVSS 126  
 Db |||||  
 140 TTVTVSS 146  
 RESULT 2  
 AAM51170  
 ID AAM51170 standard; protein; 146 AA.  
 XX  
 AC AAM51170;  
 XX  
 DT 10-JUN-2002 (first entry)  
 DE Human recombinant mAb TNV148 heavy chain variable region.  
 XX  
 KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
 KW complementarity determining region; antirheumatic; antiarthritis;  
 KW antitumor; antistatic; antiallergic; antiinflammatory; antidiabetic;  
 KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;  
 KW antianginal; cardiac; antibacterial; virucide; fungicide; antileprotic;  
 KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
 KW human; diagnosis; therapy; TNV148; monoclonal antibody; mAb.  
 XX  
 OS Homo sapiens.  
 PH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Signal\_peptide  
 FT /note= "amino acids 1-7 are PCR primer-encoded and may  
 FT differ from the native sequence"  
 FT Protein 20..146  
 FT /label= Mature\_protein  
 FT Region 31..49  
 FT /label= FR1  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 55..68  
 FT /label= FR2  
 FT Region 69..85  
 FT /label= CDR2  
 FT Region 86..117  
 FT /label= FR3  
 FT Region 118..135  
 FT /label= CDR3  
 FT Misc-difference 126  
 FT /note= "encoded by A"  
 FT Region 136..146  
 FT /label= J6  
 PN WO200212502-A2.  
 PD 14-FEB-2002.  
 XX 07-AUG-2001; 2001WO-US024785.  
 XX 07-AUG-2000; 2000US-0223360P.  
 PR 29-SEP-2000; 2000US-0236826P.  
 PR 01-AUG-2001; 2001US-00920137.  
 XX (CENZ ) CENTOCOR INC.  
 XX  
 XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
 XX WPI; 2002-217194/27.  
 DR N-PSDB; ABL53510.  
 XX  
 XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 PT angina pectoris, myocardial infarction, leprosy.  
 XX  
 PS Example 3; Fig 4; 131pp; English.  
 XX  
 CC The present sequence is that of the heavy chain variable region of anti-

CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
 CC TNV148. TNV148 was 1 of 8 human mAbs produced from a GenTNV fusion using  
 CC spleen cells from a hybrid mouse containing human variable and constant  
 CC region antibody transgenes that was immunised with human TNF alpha. The  
 CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
 CC totally human IgG1, kappa isotype. They showed relatedness to each other  
 CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The  
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
 CC humanised and/or complementarity determining region (CDR)-grafted anti-  
 CC TNF antibodies, immunoglobulins, cleavage products and other specified  
 CC portions and variants, as well as anti-TNF antibody compositions,  
 CC encoding or complementary nucleic acids, vectors, host cells,  
 CC compositions, formulations, devices, transgenic animals, transgenic  
 CC plants, and methods of making and using them. The anti-TNF antibody  
 CC comprises at least a portion of an immunoglobulin molecule, especially  
 CC the heavy chain and/or light chain variable regions given in the present  
 CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. They are useful for diagnosing or treating a TNF  
 CC related condition in a cell, tissue, organ or animal (claimed) such as  
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
 CC Creutzfeldt-Jakob disease. TNV148 may be especially useful as an  
 CC antiinflammatory

XX Sequence 146 AA;

Query Match 97.7%; Score 652.5; DB 5; Length 146;  
 Best Local Similarity 98.4%; Pred. No. 2e-48;  
 Matches 125; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 Qy 1 QQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWFAVMSYDGSNKKY 60  
 Db 20 QQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWFAVMSYDGSNKKY 79  
 Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYFCARDRGIAGCN-YYTYGMDVWGQG 119  
 Db 80 ADSVKGRFTISRDNPKNLYLQMNSLRAEDTAVYFCARDRGIAGGNTYYTYGMDVWGQG 139  
 Qy 120 TTVTVSS 126  
 Db 140 TTVTVSS 146

RESULT 3

ID AAM51169

XX AAM51169 standard; protein; 146 AA.

AC AAM51169;

XX AAM51169;

DT 10-JUN-2002 (first entry)

XX Human recombinant mAb TNV15 heavy chain variable region.

XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
 KW complementarity determining region; antirheumatic; antiarthritic;  
 KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antischlicking;  
 KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
 KW antianginal; cardiac; antibacterial; virucide; fungicide; antileprotic;  
 KW protozoacide; cycostatic; neuroprotective; antiparkinsonian; nootropic;  
 KW human; diagnosis; therapy; TNV15; monoclonal antibody; mAb.

OS Homo sapiens.

XX Key

FH Location/Qualifiers

FT Peptide  
 FT 1. 19  
 FT /label= Signal\_peptide  
 FT /note= "amino acids 1-7 are PCR primer-encoded and may  
 FT differ from the native sequence"  
 FT 20. 146  
 FT Protein  
 FT /label= Mature\_protein  
 FT 31. 49  
 FT /label= FR1  
 FT 50. 54  
 FT /label= CDR1  
 FT 55. 68  
 FT /label= FR2  
 FT 69. 85  
 FT /label= CDR2  
 FT 86. 117  
 FT /label= FR3  
 FT 118. 135  
 FT /label= CDR3  
 FT Misc-difference 126  
 FT /note= "encoded by A"  
 FT 136. 146  
 FT /label= J6

WO200212502-A2.

14-FEB-2002.

07-AUG-2001; 2001WO-US024785.

07-AUG-2000; 2000US-02233360P.

29-SEP-2000; 2000US-0236826P.

01-AUG-2001; 2001US-00920137.

XX (CENZ ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;

WPI; 2002-217194/27.

DR N-PSDB; ABL53509.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 PT angina pectoris, myocardial infarction, leprosy.

XX Example 3; Fig 4; 13lpp; English.

CC The present sequence is that of the heavy chain variable region of anti-  
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
 CC TNV15. TNV15 was 1 of 8 human mAbs produced from a GenTNV fusion using  
 CC spleen cells from a hybrid mouse containing human variable and constant  
 CC region antibody transgenes that was immunised with human TNF alpha. The  
 CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
 CC totally human IgG1, kappa isotype. They showed relatedness to each other  
 CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The  
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
 CC humanised and/or complementarity determining region (CDR)-grafted anti-  
 CC TNF antibodies, immunoglobulins, cleavage products and other specified  
 CC portions and variants, as well as anti-TNF antibody compositions,  
 CC encoding or complementary nucleic acids, vectors, host cells,  
 CC compositions, formulations, devices, transgenic animals, transgenic  
 CC plants, and methods of making and using them. The anti-TNF antibody  
 CC comprises at least a portion of an immunoglobulin molecule, especially  
 CC the heavy chain and/or light chain variable regions given in the present  
 CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. They are useful for diagnosing or treating a TNF  
 CC related condition in a cell, tissue, organ or animal (claimed) such as  
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,

CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease  
XX  
SQ Sequence 146 AA;

Query Match 93.9%; Score 627.5; DB 5; Length 146;  
Best Local Similarity 93.7%; Pred. No. 2.8e-46;  
Matches 119; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWFAFMSYDGSNKKY 60  
Db 20 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKLEWFAFMSYDGSNKKY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN-YYYGMDVWGQG 119  
Db 80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGVSAAGNYYYYGMDVWGQG 139

Qy 120 TTVTVSS 126  
Db 140 TTVTVSS 146

RESULT 4  
AAM51172  
ID AAM51172 standard; protein; 146 AA.  
AC AAM51172;  
XX  
DT 10-JUN-2002 (first entry)  
XX  
DE Human recombinant mAb TNV196 heavy chain variable region.  
XX  
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiaethmatic; antiallergic; antiinflammatory; antiscikling;  
KW antiidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antianginal; cardiac; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cycostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV196; monoclonal antibody; mAb.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal peptide  
FT /note= "amino acids 1-7 are PCR primer-encoded and may  
FT differ from the native sequence"  
FT Protein 20..146  
FT /label= Mature\_protein  
FT Region 31..49  
FT /label= FR1  
FT Region 50..54  
FT /label= CDR1  
FT Region 55..68  
FT /label= FR2  
FT Region 69..85  
FT /label= CDR2  
FT Region 86..117  
FT /label= FR3  
FT Region 118..135  
FT /label= CDR3  
FT Misc-difference 126  
FT /note= "encoded by A"  
FT Region 136..146  
FT /label= J6  
XX  
XX WO200212502-A2.  
XX  
XX 14-FEB-2002.  
XX

PF 07-AUG-2001; 2001WO-US024785.  
XX  
XX 07-AUG-2000; 2000US-0223360P.  
PR 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX  
XX (CENZ ) CENTOCOR INC.  
XX  
XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
XX  
XX WPI; 2002-217194/27.  
DR N-ESDB; ABL53512.  
XX  
XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
XX angina pectoris, myocardial infarction, leprosy.  
XX  
XX Example 3; Fig 4; 131pp; English.  
XX  
XX The present sequence is that of the heavy chain variable region of anti-  
XX tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
XX TNV196. TNV196 was 1 of 8 human mAbs produced from a GenTNV fusion using  
XX spleen cells from a hybrid mouse containing human variable and constant  
XX region antibody transgenes that was immunised with human TNF alpha. The  
XX human mAbs bound immobilised human TNF alpha with high avidity and had a  
XX totally human IgG1, kappa isotype. They showed relatedness to each other  
XX and to the human germline DP-46 heavy chain sequence (see AAM51167). The  
XX invention provides isolated human, primate, rodent, mammalian, chimeric,  
XX humanised and/or complementarity determining region (CDR)-grafted anti-  
XX TNF antibodies, immunoglobulins, cleavage products and other specified  
XX portions and variants, as well as anti-TNF antibody compositions,  
XX encoding or complementary nucleic acids, vectors, host cells,  
XX compositions, formulations, devices, transgenic animals, transgenic  
XX plants, and methods of making and using them. The anti-TNF antibody  
XX comprises at least a portion of an immunoglobulin molecule, especially  
XX the heavy chain and/or light chain variable regions given in the present  
XX sequence and in AAM51165, or either all of the CDRs of the heavy chain  
XX (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
XX 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
XX inhibit TNF binding to receptor, or provide Arthritic Index improvement  
XX in a mouse model. They are useful for diagnosing or treating a TNF  
XX related condition in a cell, tissue, organ or animal (claimed) such as  
XX rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
XX pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
XX as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
XX myocardial infarction, an infectious disease in a cell such as bacterial,  
XX viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
XX disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
XX lymphoma and multiple myeloma, or a neurological disease such as multiple  
XX sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
XX Creutzfeldt-Jakob disease  
XX  
XX Sequence 146 AA;  
SQ

Query Match 92.9%; Score 620.5; DB 5; Length 146;  
Best Local Similarity 92.9%; Pred. No. 1.1e-45;  
Matches 118; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWFAFMSYDGSNKKY 60  
Db 20 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKLEWFAFMSYDGSNKKY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN-YYYGMDVWGQG 119  
Db 80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQG 139

Qy 120 TTVTVSS 126  
Db 140 TTVTVSS 146

RESULT 5  
AAM51168

ID AAM51168 standard; protein; 146 AA.  
 XX AAM51168;  
 AC  
 DT 10-JUN-2002 (first entry)  
 XX  
 DE Human recombinant mAb TNV14 heavy chain variable region.  
 XX  
 KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
 KW complementarity determining region; antirheumatic; antiarthritic;  
 KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
 KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
 KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;  
 KW protozoacide; cycostatic; neuroprotective; antiparkinsonian; nootropic;  
 KW human; diagnosis; therapy; TNV14; monoclonal antibody; mAb.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 XX  
 FT Key  
 FT Peptide  
 FT /label= Signal\_peptide  
 FT /note= "amino acids 1-7 are PCR primer-encoded and may  
 FT differ from the native sequence"  
 FT 20..146  
 FT /label= Mature\_protein  
 FT 31..49  
 FT /label= FR1  
 FT 50..54  
 FT /label= CDR1  
 FT 55..68  
 FT /label= FR2  
 FT 69..85  
 FT /label= CDR2  
 FT 86..117  
 FT /label= FR3  
 FT 118..135  
 FT /label= CDR3  
 FT Misc-difference 126  
 FT /note= "encoded by A"  
 FT 136..146  
 FT /label= J6  
 XX  
 FN WO200212502-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PP 07-AUG-2001; 2001WO-US024785.  
 XX  
 PR 07-AUG-2000; 2000US-0223360P.  
 PR 29-SEP-2000; 2000US-0236826P.  
 PR 01-AUG-2001; 2001US-00920137.  
 XX  
 PA (CENZ ) CENTOCOR INC.  
 XX  
 XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
 PI WPI; 2002-217194/27.  
 DR N-PSDB; ABL53508.  
 XX  
 XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 PT angina pectoris, myocardial infarction, leprosy.  
 XX  
 PS Example 3; Fig 4; 131pp; English.  
 XX  
 CC The present sequence is that of the heavy chain variable region of anti-  
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
 CC TNV14. TNV14 was 1 of 8 human mAbs produced from a GenTmV fusion using  
 CC spleen cells from a hybrid mouse containing human variable and constant  
 CC region antibody transgenes that was immunised with human TNF alpha. The  
 CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
 CC totally human IgG1, kappa isotype. They showed relatedness to each other  
 CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The

CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
 CC humanised and/or complementarity determining region (CDR)-grafted anti-  
 CC TNF antibodies, immunoglobulins, cleavage products and other specified  
 CC portions and variants, as well as anti-TNF antibody compositions,  
 CC encoding or complementary nucleic acids, vectors, host cells,  
 CC compositions, formulations, devices, transgenic animals, transgenic  
 CC plants, and methods of making and using them. The anti-TNF antibody  
 CC comprises at least a portion of an immunoglobulin molecule, especially  
 CC the heavy chain and/or light chain variable regions given in the present  
 CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. They are useful for diagnosing or treating a TNF  
 CC related condition in a cell, tissue, organ or animal (claimed) such as  
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
 CC Creutzfeldt-Jakob disease  
 XX  
 XX Sequence 146 AA;  
 SQ  
 Query Match 92.1%; Score 615.5; DB 5; Length 146;  
 Best Local Similarity 92.9%; Pred. No. 3e-45;  
 Matches 118; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 QVQLVESGGGVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGKGLVAFWYSDGSNKKY 60  
 DB 20 QVQLVESGGGVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGKGLVAFWYSDGSNKKY 79  
 QY 61 ADSVKGRFTISRDN SKNTLYLQMSLR AEDTAVYVCARDRGIAAGN-YYTYGMDVWGQ 119  
 DB 80 ADSVKDRFTISRDN SKNTLYLQMSLR AEDTAVYVCARDRGISAGNYYTYGMDVWGQ 139  
 QY 120 TTVTVSS 126  
 DB 140 TTVTVSS 146  
 RESULT 6  
 ADD28320  
 ID ADD28320 standard; protein; 135 AA.  
 XX  
 AC ADD28320;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:98.  
 XX  
 KW human heterodimeric antibody; human; antibody; binding affinity;  
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
 KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;  
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003076568-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PP 11-FEB-2003; 2003WO-US004206.  
 XX  
 PR 11-FEB-2002; 2002US-0356086P.  
 PR 29-APR-2002; 2002US-0376408P.  
 PR 27-SEP-2002; 2002US-0414053P.  
 PR 25-NOV-2002; 2002US-0428807P.

```

XX (ALEX-) ALEXION PHARM INC.
XX PA Bowdish KS, Wild MA;
XX PI WPI; 2003-722327/68.
XX DR
XX PT New human heterodimeric antibodies or their antibody fragments, useful as
XX PT anti-toxins or anti-infectives with respect to infective agents, e.g.
XX PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
XX PT Nile virus.
XX PS Claim 11; SEQ ID NO 98; 67pp; English.
XX CC The present invention describes a human heterodimeric antibody (I)
XX CC (fragment) having a binding affinity of at least 1x10-8 M to the
XX CC protective antigen of Bacillus anthracis or a molecule involved in
XX CC anthrax infection that blocks binding of the antigen or molecule to cell
XX CC receptors, edema factor and lethal factor. (I) has virucide and
XX CC antibacterial activities, and can be used in immunotherapy. The
XX CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
XX CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
XX CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
XX CC present sequence represents a human heterodimeric antibody heavy chain
XX CC variable region amino acid sequence, which is used in the exemplification
XX CC of the present invention.
XX SQ Sequence 135 AA;

Query Match 87.3%; Score 583; DB 7; Length 135;
Best Local Similarity 86.7%; Pred. No. 1.7e-42;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGRSRLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 EVQLVESGGGVVQPGRSRLRLSCAASGFIFFSSYGLHWVRQAPGKLEWVAFISYDGSKNKY 62
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN--YYYYGMDVWGQ 118
DB 63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDRVIVPAANKYIIYYGMDVWGQ 122
QY 119 GTTIVTSS 126
DB 123 GTTIVTSS 130

RESULT 7
ADD28236
XX ID ADD28236 standard; protein; 135 AA.
XX AC ADD28236;
XX DT 15-JAN-2004 (first entry)
XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:14.
XX KW human heterodimeric antibody; human; antibody; binding affinity;
XX KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
XX KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
XX KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX OS Synthetic.
XX OS Homo sapiens.
XX FN WO2003076568-A2.
XX PD 18-SEP-2003.
XX PF 11-FEB-2003; 2003WO-US004206.
XX PR 11-FEB-2002; 2002US-0356086P.
XX PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414053P.
PR 25-NOV-2002; 2002US-0428807P.
XX (ALEX-) ALEXION PHARM INC.
XX PA Bowdish KS, Wild MA;
XX PI WPI; 2003-722327/68.
XX DR
XX PT New human heterodimeric antibodies or their antibody fragments, useful as
XX PT anti-toxins or anti-infectives with respect to infective agents, e.g.
XX PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
XX PT Nile virus.
XX PS Claim 6; SEQ ID NO 14; 67pp; English.
XX CC The present invention describes a human heterodimeric antibody (I)
XX CC (fragment) having a binding affinity of at least 1x10-8 M to the
XX CC protective antigen of Bacillus anthracis or a molecule involved in
XX CC anthrax infection that blocks binding of the antigen or molecule to cell
XX CC receptors, edema factor and lethal factor. (I) has virucide and
XX CC antibacterial activities, and can be used in immunotherapy. The
XX CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
XX CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
XX CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
XX CC present sequence represents a human heterodimeric antibody heavy chain
XX CC variable region amino acid sequence, which is used in the exemplification
XX CC of the present invention.
XX SQ Sequence 135 AA;

Query Match 87.3%; Score 583; DB 7; Length 135;
Best Local Similarity 86.7%; Pred. No. 1.7e-42;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGRSRLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 EVQLVESGGGVVQPGRSRLRLSCAASGFIFFSSYGLHWVRQAPGKLEWVAFISYDGSKNKY 62
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN--YYYYGMDVWGQ 118
DB 63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDRVIVPAANKYIIYYGMDVWGQ 122
QY 119 GTTIVTSS 126
DB 123 GTTIVTSS 130

RESULT 8
ADV86823
XX ID ADV86823 standard; protein; 135 AA.
XX AC ADV86823;
XX DT 10-MAR-2005 (first entry)
XX DE Bacillus anthracis toxin Fab 9 K 2h G pro heavy chain variable region.
XX KW Bioterrorism; Bacillus anthracis infection; vaccine; diagnosis;
XX KW antibacterial; antibody; heavy chain variable region.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 26 /note= "Unidentified residue"
XX FT WO2004110362-A2.
XX PN 23-DEC-2004.
XX PD 26-MAY-2004; 2004WO-US016557.
XX PR

```









QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN-YYTGMVMDVWGQ 119  
 Db 202 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN-YYTGMVMDVWGQ 261  
 QY 120 TTVTVSS 126  
 Db 262 TTVTVSS 268

RESULT 14  
 AAY44995  
 ID AAY44995 standard; protein; 524 AA.  
 AC AAY44995;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE HD70scFv-Ck-interleukin 2.  
 KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
 KW EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; Ck-domain; kappa light chain constant domain;  
 KW heteromultimer; multifunctional compound; immunoglobulin; cytostatic;  
 KW immunostimulatory; antileukemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200006605-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 28-JUL-1999; 99WO-EP005416.  
 XX  
 PR 28-JUL-1999; 98EP-00114082.  
 XX  
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 XX  
 PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;  
 XX  
 DR WPI; 2000-195265/17.  
 DR N-PSDB; AAZ50588.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 FS Example 10; Fig 55B; 166pp; English.  
 XX  
 CC The patent discloses heteromultimers which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CHI-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromultimers have  
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the right chain of a  
 CC heteromultimer comprising HD70 single-chain Fv (scFv) fragment N-  
 CC terminally linked to human Ck domain (constant domain of immunoglobulin-  
 CC kappa light chain) which bears at its C-terminus the human inflammatory  
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the  
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen  
 XX  
 SQ Sequence 524 AA;

Query Match 87.1%; Score 581.5; DB 3; Length 524;

Best Local Similarity 87.4%; Pred. No. 9.3e-42;  
 Matches 111; Conservative 5; Mismatches 10; Indels 1; Gaps 1;  
 QY 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
 Db 142 EVQLLESGGGVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 201  
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN-YYTGMVMDVWGQ 119  
 Db 202 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN-YYTGMVMDVWGQ 261  
 QY 120 TTVTVSS 126  
 Db 262 TTVTVSS 268

RESULT 15  
 ADK18593  
 ID ADK18593 standard; protein; 126 AA.  
 AC ADK18593;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody heavy chain protein sequence.  
 XX  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 PT New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 FS Disclosure; SEQ ID NO 17; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.  
 XX  
 SQ Sequence 126 AA;

Query Match 87.0%; Score 581; DB 7; Length 126;  
 Best Local Similarity 88.1%; Pred. No. 2.4e-42;  
 Matches 111; Conservative 3; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
 Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN-YYTGMVMDVWGQ 120

|||||  
61 ADSVKGRFTISRDNKNTLYLOMNSLRABDTAVYYCARDQGYRAGYYDYGMQGT 120  
Qy 121 TTVSS 126  
|||  
Db 121 TTVSS 126

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Job time : 149.538 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:46:34 ; Search time 25.8462 Seconds  
(without alignments)  
469.057 Million cell updates/sec

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Perfect score: 668  
Sequence: 1 QVQLVSGGGVQPSRL.....NYTYGMDVWGQTTVTSS 126

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	86.4	122	2 E36005	Ig heavy chain V r
2	575	86.1	128	2 S48797	Ig heavy chain V r
3	563.5	84.4	123	2 S38493	Ig heavy chain - h
4	539.5	80.8	119	2 P36005	Ig heavy chain V r
5	537	80.4	118	2 S31116	Ig heavy chain - h
6	534.5	80.0	121	2 G36005	Ig heavy chain V r
7	533	79.8	147	2 I37780	Ig variable region
8	532.5	79.7	133	2 A49028	Ig heavy chain V-I
9	532	79.6	114	2 S46390	Ig heavy chain V r
10	530.5	79.4	132	2 S31603	Ig heavy chain V r
11	529.5	79.3	121	2 S19666	Ig heavy chain V r
12	528.5	79.1	134	2 S31679	Ig heavy chain V r
13	528	79.0	140	2 S70442	Ig heavy chain pre
14	524	78.4	114	2 S46392	Ig heavy chain V r
15	524	78.4	122	2 S31117	Ig heavy chain - h
16	519	77.7	120	2 S31112	Ig heavy chain - h
17	515.5	77.2	160	2 S05271	Ig heavy chain pre
18	515	77.1	118	2 PH1660	Ig heavy chain V r
19	514	76.9	137	2 S31701	Ig heavy chain V r
20	514	76.9	139	2 S31674	Ig heavy chain V r
21	512.5	76.7	130	2 PL0098	Ig heavy chain pre
22	511.5	76.6	125	2 S37455	Ig mu chain - huma
23	510.5	76.4	130	2 S31601	Ig heavy chain V r
24	509.5	76.3	135	2 S31598	Ig heavy chain V r
25	507.5	76.0	117	2 S36259	Ig heavy chain V-I
26	507	75.9	122	1 M3HUAM	Ig heavy chain V r
27	504.5	75.5	111	2 PH1645	Ig heavy chain V r
28	503	75.3	114	2 S46391	Ig heavy chain V r
29	499.5	74.8	117	2 S36270	Ig heavy chain V r

30	499	74.7	133	2 S31510	Ig heavy chain - h
31	495.5	74.2	109	2 PH1646	Ig heavy chain V r
32	494.5	74.0	109	2 PH1644	Ig heavy chain V r
33	494.5	74.0	123	2 S26794	Ig heavy chain V r
34	493	73.8	118	2 PH1662	Ig heavy chain V r
35	493	73.8	126	1 GIHUKL	Ig heavy chain V-I
36	492	73.7	145	2 S11239	Ig heavy chain V r
37	491.5	73.6	113	2 S38490	Ig heavy chain - h
38	490	73.4	151	2 A60943	Ig heavy chain pre
39	489.5	73.3	122	2 S31119	Ig heavy chain - h
40	489	73.2	108	2 PH1642	Ig heavy chain V r
41	487.5	73.0	119	2 S31107	Ig heavy chain - h
42	487.5	73.0	121	2 PH1661	Ig heavy chain V r
43	487.5	73.0	125	2 S30531	Ig heavy chain V r
44	486.5	72.8	111	2 PH1643	Ig heavy chain V r
45	485.5	72.7	127	2 S38489	Ig heavy chain - h

## ALIGNMENTS

## RESULT 1

E36005

Ig heavy chain V region (M72) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998

C/Accession: E36005

R/Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: E36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122 <SCH>

A/Cross-references: UNIPARC:UPI0000176C30; GB:M34030

C/Genetics:

A/Gene: GDB:IGH@; IGHDY1

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	86.4%;	Score	577;	DB 2;	Length	122;			
Best Local Similarity	88.9%;	Pred. No.	6.9e-45;						
Matches	112;	Conservative	4;	Mismatches	6;	Indels	4;	Gaps	1
Qy	1	QVQLVESGGGVQPSRLSLSCAASGFTFSYAMHWVQAPGNGLEWFAWFSYDGSNKY	60						
Db	1	QVQLVESGGGVQPSRLSLSCAASGFTFSYAMHWVQAPGNGLEWFAWFSYDGSNKY	60						
Qy	61	ADSVKGRFTISRDNSKNTLYQMNSLRADTAVYYCARDRIAGGNTYYGMDVWGQGT	120						
Db	61	ADSVKGRFTISRDNSKNTLYQMNSLRADTAVYYCARDRIAGGNTYYGMDVWGQGT	116						
Qy	121	TVTVSS	126						
Db	117	TVTVSS	122						

## RESULT 2

S48797

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Sep-1998 #text\_change 23-Jul-1999

C/Accession: S48797; S26893

R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A/Description: Molecular characterization of natural human anti-Sm autoantibodies.

A/Reference number: S48797

A/Accession: S48797

A/Molecule type: mRNA

A;Residues: 1-128 <MA>  
A;Cross-references: UNIPARC:UPI0000116700; EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A;Reference number: S26885; MUID:93021117; PMID:1404388  
A;Accession: S26893  
A;Molecule type: DNA  
A;Residues: 1-98 <TOM>  
A;Cross-references: UNIPARC:UPI0000038183; EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 86.1%; Score 575; DB 2; Length 128;  
Best Local Similarity 87.5%; Pred. No. 1.1e-44; Mismatches 11; Indels 2; Gaps 1;  
Matches 112; Conservative 3; Mismatches 11; Indels 2; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGKLEWVAVIWDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRI--AAGNYYTYGMDVWGQ 118  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDNYTSSGYYTYTYGMDVWGQ 120  
  
Qy 119 GTTVTVSS 126  
Db 121 GTTVTVSS 128  
  
RESULT 3  
S38493  
Ig heavy chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S38493  
R;Marks, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S  
submitted to the EMBL Data Library, June 1993  
A;Description: Human antibody fragments specific for human blood group antigens from a P  
A;Reference number: S38488  
A;Accession: S38493  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-123 <MA>  
A;Cross-references: UNIPARC:UPI000011654F; EMBL:Z23036; NID:G414033; PIDN:CAA80571.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 84.4%; Score 563.5; DB 2; Length 123;  
Best Local Similarity 87.3%; Pred. No. 1.1e-43; Mismatches 10; Indels 3; Gaps 1;  
Matches 110; Conservative 3; Mismatches 10; Indels 3; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGKLEWVAVIWDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAGAGNYYTYGMDVWGQ 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARAR---SNWNYTYTYGMDVWGKT 117  
  
Qy 121 TTVTVSS 126  
Db 118 TTVTVSS 123  
  
RESULT 4  
F36005  
Ig heavy chain V region (M49) - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 31-Dec-2004  
C;Accession: F36005

R;Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A;Reference number: A36005; MUID:90349571; PMID:2117273  
A;Accession: F36005  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-119 <SCH>  
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026  
C;Genetics:  
A;Gene: GDB:IGH@; IGHDY1  
A;Cross-references: GDB:118731; OMIM:146910  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 80.8%; Score 539.5; DB 2; Length 119;  
Best Local Similarity 84.1%; Pred. No. 1.5e-41; Mismatches 106; Conservative 3; Mismatches 10; Indels 7; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGKLEWVAVIWDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAGAGNYYTYGMDVWGQ 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRKASD-----AFDIWGQGT 113  
  
Qy 121 TTVTVSS 126  
Db 114 MVTVSS 119  
  
RESULT 5  
S31116  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
C;Accession: S31116  
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A;Reference number: S31104; MUID:92111633; PMID:1730252  
A;Accession: S31116  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-118 <RAA>  
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966  
C;Superfamily: immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 80.4%; Score 537; DB 2; Length 118;  
Best Local Similarity 84.1%; Pred. No. 2.6e-41; Mismatches 106; Conservative 2; Mismatches 10; Indels 8; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSSYAMHWVRQAPGKLEWVAVIWDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAGAGNYYTYGMDVWGQ 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCATDGGKAA-----FDIWGQGT 112  
  
Qy 121 TTVTVSS 126  
Db 113 MVTVSS 118  
  
RESULT 6  
G36005

Ig heavy chain V region (M74) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 31-Dec-2004  
C:Accession: G36005  
R:Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A36005; MUID:90349571; PMID:2117273  
A:Accession: G36005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-121 <SCH>  
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34031  
C:Genetics:  
A:Gene: GDB:IGH; IGHV1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
A:Superfamily: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 534.5; DB 2; Length 121;  
Best Local Similarity 84.1%; Pred. No. 4.4e-41;  
Matches 106; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFWVSFDGSNKKY 60  
Db 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAVISYDGSNKKY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRTAAGNNYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDR-----KDWGNAIFDYWGQGT 115  
  
Qy 121 TVTVSS 126  
Db 116 LVTVSS 121

RESULT 7  
137780  
Ig variable region (VDJ) (clone T20-11) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 23-Jul-1999  
C:Accession: 137780; S25474  
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: 137780  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <RES>  
A:Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 533; DB 2; Length 147;  
Best Local Similarity 83.3%; Pred. No. 7.3e-41;  
Matches 105; Conservative 4; Mismatches 15; Indels 2; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFWVSFDGSNKKY 60  
Db 14 EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYMSWVRQAPGKLEWVANIKQDSEKYY 73  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRTAAGNNYYGMDVWGQGT 120  
Db 74 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKDG--EGWGLYYGMDVWGQGT 131  
  
Qy 121 TVTVSS 126  
Db 132 TVTVSS 137

RESULT 8  
A49028  
Ig heavy chain V-III region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C:Accession: A49028  
R:Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur  
Eur. J. Immunol. 21, 2355-2363, 1991  
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lympho  
A:Reference number: A49028; MUID:92008140; PMID:1915549  
A:Accession: A49028  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-133 <TIM>  
A:Cross-references: UNIPARC:UPI0000113P2C; GB:S64471; NID:G236904; PIDN:AAB20011.1; PID  
A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines  
A:Note: sequence extracted from NCBI backbone (NCBI:64471, NCBIP:64470)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 532.5; DB 2; Length 133;  
Best Local Similarity 83.6%; Pred. No. 7.3e-41;  
Matches 107; Conservative 2; Mismatches 12; Indels 7; Gaps 2;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFWVSFDGSNKKY 60  
Db 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYMHVLRQAPGKLEWVAVIWDGSNKKY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDR--GTAAGNNYYGMDVWGQ 118  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRLTIAAGNF-----DYWGQ 115  
  
Qy 119 GTTVTSS 126  
Db 116 GTLATVSS 123

RESULT 9  
S46390  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46390  
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46390  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>  
A:Cross-references: UNIPARC:UPI000011663F; EMBL:Z31686; NID:G509782; PIDN:CAA83491.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 532; DB 2; Length 114;  
Best Local Similarity 83.3%; Pred. No. 6.9e-41;  
Matches 105; Conservative 2; Mismatches 7; Indels 12; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFWVSFDGSNKKY 60  
Db 1 EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYMHVLRQAPGKLEWVAVISYDGSNKKY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRTAAGNNYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDWG-----DYWGQGT 108  
  
Qy 121 TVTVSS 126  
Db 109 LVTVSS 114

```
RESULT 10
S31603
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31603
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31603
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: UNIPARC:UPI0000116455; EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 530.5; DB 2; Length 132;
Best Local Similarity 82.5%; Pred. No. 1.1e-40;
Matches 104; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

Qy 1 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYAMHVRQAPGNGLEWVAFMSYDGSNKYY 60
Db 16 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYAMHVRQAPGKLEWVAVISYDGSNKYY 75

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAGGNTYYTGMVWGQGT 120
Db 76 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDL-----FYFF--DYWGQGT 126

Qy 121 TVTVSS 126
Db 127 LVTVSS 132

RESULT 11
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Marks, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MAR>
A:Cross-references: UNIPARC:UPI0000115PE5; EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 529.5; DB 2; Length 121;
Best Local Similarity 82.5%; Pred. No. 1.2e-40;
Matches 104; Conservative 6; Mismatches 11; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYAMHVRQAPGNGLEWVAFMSYDGSNKYY 60
Db 1 QVQLVQSGGGVQPGSRSLRLSCAASGTFISFYGMHVRQAPGKLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAGGNTYYTGMVWGQGT 120
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK-TGYSGWGYP----DYWGQGT 115

Qy 121 TVTVSS 126
Db 116 LVTVSS 121

RESULT 12
S46392
Ig heavy chain V region (VH-28) - human
```

```
S31679
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31679
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31679
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>
A:Cross-references: UNIPARC:UPI0000116475; EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 528.5; DB 2; Length 134;
Best Local Similarity 83.5%; Pred. No. 1.7e-40;
Matches 106; Conservative 2; Mismatches 6; Indels 13; Gaps 2;

Qy 1 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYAMHVRQAPGNGLEWVAFMSYDGSNKYY 60
Db 20 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYAMHVRQAPGKLEWVAVISYDGSNKYY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARD-RGIAAGNYYTGMVWGQGT 119
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARESG-----DYWGQGT 127

Qy 120 TVTVSS 126
Db 128 LTVTVSS 134

RESULT 13
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
C:Accession: S70442
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda BSV human B cell clone: an early step of differentiation of f
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70442
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176EB7
C:Superfamily: immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 528; DB 2; Length 140;
Best Local Similarity 82.5%; Pred. No. 2e-40;
Matches 104; Conservative 3; Mismatches 13; Indels 6; Gaps 2;

Qy 1 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYAMHVRQAPGNGLEWVAFMSYDGSNKYY 60
Db 20 QVQLVESGGGVQPGSRSLRLSCAASGTFISFYGMHVRQAPGKLEWVAVIRYDGSNKYY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAGGNTYYTGMVWGQGT 120
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAEDH---IVGATYF----DYWGQGT 133

Qy 121 TVTVSS 126
Db 134 LTVTVSS 139

RESULT 14
S46392
Ig heavy chain V region (VH-28) - human
```



C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46392  
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46392  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>  
A:Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:9499306; PIDN:CAA83493.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 524; DB 2; Length 114;  
Best Local Similarity 82.5%; Pred. No. 3.6e-40;  
Matches 104; Conservative 1; Mismatches 9; Indels 12; Gaps 1;  
  
Qy 1 QVQLVESGGVVQPGSRLLRSCAASGFTIFSSYAMHWVRQAPGNGLEWVAFMYSYDGSNKYY 60  
Db 1 QVNLRESGGVVQPGSRLLRSCAASGFTIFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNTYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDSG-----GYWGQGT 108  
  
Qy 121 TTVTSS 126  
Db 109 TTVTSS 114

RESULT 15  
S31117  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31117  
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31117  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <RAA>  
A:Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 524; DB 2; Length 122;  
Best Local Similarity 83.3%; Pred. No. 3.9e-40;  
Matches 105; Conservative 4; Mismatches 13; Indels 4; Gaps 2;  
  
Qy 1 QVQLVESGGVVQPGSRLLRSCAASGFTIFSSYAMHWVRQAPGNGLEWVAFMYSYDGSNKYY 60  
Db 1 QVQLVESGGVVQPGSRLLRSCAASGFTIFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNTYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD--FFAPPNNSHP--DYWGQGT 116  
  
Qy 121 TTVTSS 126  
Db 117 LTVTSS 122

Search completed: December 28, 2005, 14:04:02  
Job time : 26.8462 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension .rnp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:44:24 ; Search time 159.923 Seconds  
(without alignments)  
555.871 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QVQLVSGGGVQVQPSRLR.....NYYTGMVGVGGTTVTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05\_80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528	79.0	613	2 Q8WUK1_HUMAN	Q8wuk1 homo sapien
2	520.5	77.9	472	2 Q8N089_HUMAN	Q8n089 homo sapien
3	518.5	77.6	116	2 Q8UL93_HUMAN	Q8ul93 homo sapien
4	518	77.5	606	2 Q6GMY2_HUMAN	Q6gmy2 homo sapien
5	514.5	77.0	240	2 Q65ZC9_HUMAN	Q65zc9 homo sapien
6	513.5	76.9	113	2 Q8UL90_HUMAN	Q8ul90 homo sapien
7	510	76.3	573	2 Q8WU38_HUMAN	Q8wu38 homo sapien
8	507	75.9	122	1 HV33G_HUMAN	P01768 homo sapien
9	503	75.3	147	2 Q9Y509_HUMAN	Q9y509 homo sapien
10	501.5	75.1	478	2 Q6PI81_HUMAN	Q6pi81 homo sapien
11	493	73.8	126	1 HV3K_HUMAN	P01772 homo sapien
12	485	72.6	122	2 Q8UL84_HUMAN	Q8ul84 homo sapien
13	484.5	72.5	597	2 Q6BB9_HUMAN	Q6bb9 homo sapien
14	480	71.9	544	2 Q6PJ95_HUMAN	Q6pj95 homo sapien
15	479	71.7	122	1 HV3H_HUMAN	P01769 homo sapien
16	479	71.7	469	2 Q569F4_HUMAN	Q569f4 homo sapien
17	477.5	71.5	119	1 HV3J_HUMAN	P01770 homo sapien
18	475.5	71.2	464	2 Q6MZU6_HUMAN	Q6mzu6 homo sapien
19	475.5	71.2	470	2 Q6PJ44_HUMAN	Q6pj44 homo sapien
20	470.5	70.4	121	2 Q8UL71_HUMAN	Q8ul71 homo sapien
21	470	70.4	136	1 HV16_MOUSE	P01783 mus musculus
22	469.5	70.3	121	1 HV3J_HUMAN	P01771 homo sapien
23	465	69.6	475	2 Q8EFE5_HUMAN	Q8efe5 homo sapien
24	463.5	69.4	493	2 Q6GMX2_HUMAN	Q6gmx2 homo sapien
25	463.5	69.4	519	2 Q6N092_HUMAN	Q6n092 homo sapien
26	459.5	68.8	493	2 Q8NCL6_HUMAN	Q8nc16 homo sapien
27	459.5	68.8	499	2 Q8N5K4_HUMAN	Q8n5k4 homo sapien
28	457	68.4	467	2 Q4VBH1_RAT	Q4vbh1 rattus norv
29	452	67.7	465	2 Q5I0J0_RAT	Q5i0j0 rattus norv
30	451	67.5	118	2 Q9UL91_HUMAN	Q9ul91 homo sapien
31	450.5	67.4	482	2 Q7Z351_HUMAN	Q7z351 homo sapien

#### RESULT 1

ID	Q8WUK1_HUMAN	HUMAN	PRELIMINARY;	PRT;	613 AA.
AC	Q8WUK1				
DT	01-MAR-2002	(TrEMBLrel. 20, Created)			
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	IGHM protein.				
GN	Name=IGHM;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Primary B-Cells;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,				
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RL	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Primary B-Cells;				
RG	NIH MGC Project;				
RL	Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.				
RL	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RX	PubMed=2117273;				
RA	Schroeder H.W. Jr, Wang J.Y.;				
RT	"Preferential utilization of conserved immunoglobulin heavy chain				
RT	variable gene segments during human fetal life."				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).				
RL	[4]				
RP	NUCLEOTIDE SEQUENCE.				
RX	PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;				
RA	Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;				

32	450	67.4	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien
33	446	66.8	475	2	Q6GMW7_HUMAN	Q6gmw7 homo sapien
34	445	66.6	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
35	443	66.3	116	1	HV3T_HUMAN	P01781 homo sapien
36	443	66.3	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
37	441.5	66.1	470	2	Q68CN4_HUMAN	Q68cn4 homo sapien
38	441	66.0	118	2	Q9UL72_HUMAN	Q9ul72 homo sapien
39	439.5	65.8	479	2	Q5BK12_RAT	Q5bk12 rattus norv
40	437	65.4	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
41	436	65.3	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
42	436	65.3	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
43	436	65.3	487	2	Q99KA4_MOUSE	Q99ka4 mus musculus
44	436	65.3	494	2	Q96K68_HUMAN	Q96k68 homo sapien
45	435.5	65.2	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculus

#### ALIGNMENTS



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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.B., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RA "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336 (1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2840480;
RA Bird J., Gallili N., Link M., Stites D., Sklar J.;
RT "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia.";
RL J. Exp. Med. 168:229-245 (1988).
RL EMBL; AF035021; AAD56257.1; -, mRNA.
DR PIR; PH1644; PH1644.
DR PIR; PLO120; PLO120.
DR HSSP; P01772; 2PB4.
DR SMR; O9UL93; 1-116.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
FT NON TER 1
FT NON TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 77.6%; Score 518.5; DB 2; Length 116;
Best Local Similarity 81.6%; Pred. No. 2.9e-44;
Matches 102; Conservative 4; Mismatches 10; Indels 9; Gaps 1;

Qy 2 VOLVESGGGVQPGRSRLSCAASGFISSYAMHWVRQAPGNGLEWAFMSYDGSNKKYA 61
Db 1 VOLVESGGGVQPGRSRLSCAASGFISSYAMHWVRQAPGNGLEWAFMSYDGSNKKYA 60

Qy 62 DSVKGRFTISRDNKNTLYLQWNSLRADTVAVYCARDRGIAAGNYYYGMDVWGQGT 121
Db 61 DSVKGRFTISRDNKNTLYLQWNSLRADTVAVYCARDRGIAAGNYYYGMDVWGQGT 111

Qy 122 VTSS 126
Db 112 VTSS 116

RESULT 4
Q6GMV2 HUMAN PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.

NCBI_TaxID=9606;
OX [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073758; AAH73758.1; -, mRNA.
DR SMR; Q6GMV2; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 606 AA; 66185 MW; B6538B51114B4C55 CRC64;

Query Match 77.5%; Score 518; DB 2; Length 606;
Best Local Similarity 76.1%; Pred. No. 2.2e-43;
Matches 102; Conservative 8; Mismatches 16; Indels 8; Gaps 2;

Qy 1 QVLVESGGGVQPGRSRLSCAASGFISSYAMHWVRQAPGNGLEWAFMSYDGSNKKY 60
Db 20 QVLVESGGGVQPGRSRLSCAASGFISSYAMHWVRQAPGNGLEWAFMSYDGSNKKY 79

Qy 61 ADSVKGRTISRDNKNTLYLQWNSLRADTVAVYCAR-DRGIAAGN-----YYYYG 112
Db 80 ADSVKGRTISRDNKNTLYLQWNSLRADTVAVYCAR-DRGIAAGN-----YYYYG 139

Qy 113 MDVWGQGTTVTVSS 126
Db 140 MDVWGQGTTVTVSS 153

RESULT 5
Q65ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C1G/7;  
 RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RL "Complement recruitment using bispecific diabodies.";  
 RT Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL; Y13056; CAA73499.1; -; mRNA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 FT NON TER 1  
 FT NON TER 240 240  
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;  
 Query Match 77.0%; Score 514.5; DB 2; Length 240;  
 Best Local Similarity 80.2%; Pred. No. 1.7e-43;  
 Matches 101; Conservative 6; Mismatches 10; Indels 9; Gaps 1;  
 QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKGLVWVAFMSYDGSNKYY 60  
 DB 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFSYGMHWVRQAPKGLVWVAFVSYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQGT 120  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDWGS-----LDPWGKGT 111  
 QY 121 TVTVSS 126  
 DB 112 LVTWSS 117  
 RESULT 6  
 Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.  
 AC Q9UL90;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/glin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
 RL Clin. Immunol. 87:184-192 (1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1730252;  
 RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
 RA Schuurman R.K.;  
 RT "Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.";  
 RL Eur. J. Immunol. 22:247-251(1992).  
 DR EMBL; AF035024; AAD56260.1; -; mRNA.  
 DR PIR; S78486; S78486.  
 DR HSSP; P01772; 2FB4.  
 DR SMR; Q9UL90; 1-113.

DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 FT NON TER 1  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;  
 Query Match 76.9%; Score 513.5; DB 2; Length 113;  
 Best Local Similarity 79.4%; Pred. No. 9e-44; 5; Mismatches 13; Gaps 1;  
 Matches 100; Conservative 5;  
 QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKGLVWVAFMSYDGSNKYY 60  
 DB 1 EVQLVESGGGVVQPGSLRLSCAASGFTFSYGMHWVRQAPKGLVWVAFIRYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQGT 120  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD-----LNYWGQGT 107  
 QY 121 TVTVSS 126  
 DB 108 LVTWSS 113  
 RESULT 7  
 Q8WU38 HUMAN PRELIMINARY; PRT; 573 AA.  
 ID Q8WU38 HUMAN PRELIMINARY;  
 AC Q8WU38;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGH domain protein.  
 GN Name=IGHD;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J.J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RA Director MGC Project;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=1555592;  
 RA Makiya R., Stigbrand T.;  
 RT "Placental alkaline phosphatase has a binding site for the human



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RT immunoglobulin-G Fc portion."
RL Eur. J. Biochem. 205:341-345(1992).
DR EMBL; BC021276; AAH21276.1; -; mRNA.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSSP; P18529; I18K.
DR Ensembl; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 76.3%; Score 510; DB 2; Length 573;
Best Local Similarity 76.6%; Pred. No. 1.3e-42;
Matches 98; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGTFIPSSYAMHWVRQAPGNGLEWVAFWMSYDGSNKKY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EQVLVESGGGVVQPGKSLRLSCAASGTFIPSSYAMHWVRQAPGNGLEWVAFWMSYDGSNKKY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNY--YYGMDVWGQ 118
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNY--GSIGIYYGMDVWGQ 135

Qy 119 GTTVTVSS 126
Db :|||||:
136 GTTVTVSS 143

RESULT 8
HV3G HUMAN STANDARD; PRT; 122 AA.
AC P01768;
AT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W.; Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC patient with macroglobulinemia.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02051; M3HUAM.
CC HSSP; P01772; 2PBA.
CC SMR; P01768; 2-122.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 112 Ig-like.
FT MOD_RES 1 122 Pyrrolidone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 75.9%; Score 507; DB 1; Length 122;
Best Local Similarity 76.2%; Pred. No. 4.5e-43;
Matches 96; Conservative 14; Mismatches 12; Indels 4; Gaps 2;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGTFIPSSYAMHWVRQAPGNGLEWVAFWMSYDGSNKKY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVELVESGGGVVQPGKSLRLSCAASGTFIPSSYAMHWVRQAPGNGLEWVAFWMSYDGSNKKY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQ 116

Qy 121 TTVTVSS 126
Db :|||||:
117 TTVTVSS 122

RESULT 9
QY509 HUMAN PRELIMINARY; PRT; 147 AA.
ID QY509 HUMAN PRELIMINARY; PRT; 147 AA.
AC QY509;
AT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH3 protein (Fragment).
GN Name=VH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J.; Vesco R.A.; Rettig M.B.; Hong C.H.; Kim A.; Lee J.C.;
RA Lichtenstein A.K.; Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1348-1353(1995).
DR EMBL; S80860; AADI4339.1; -; mRNA.
DR HSSP; P01842; 1AQK.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 75.3%; Score 503; DB 2; Length 147;
Best Local Similarity 76.2%; Pred. No. 1.4e-42;
Matches 96; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGTFIPSSYAMHWVRQAPGNGLEWVAFWMSYDGSNKKY 60
Db 1 QVHLVESGGGVVQPGKSLRLSCAASGTFIPSSYAMHWVRQAPGKGLDWALLSIDGSTQY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AGSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQ 120

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FT STRAND 68 73
  TURN 74 77
  FT STRAND 78 83
  FT STRAND 83 90
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  FT STRAND 92 99
  FT STRAND 106 106
  FT STRAND 107 108
  FT STRAND 109 109
  FT STRAND 113 116
  FT STRAND 120 124
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 73.8%; Score 493; DB 1; Length 126;
Best Local Similarity 76.2%; Pred. No. 1.2e-41;
Matches 96; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Oy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFIFFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db 1 QVQLVESGGGVVQPGSRSLRLSCSSGGFIFFSYAMWVRQAPGKLEWVAIITWDGSDQHY 60

Oy 61 ADSVKGRTTIFRDNSKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYTYYGMDVWGQGT 120
Db 61 ADSVKGRTTIFRDNSKNTLYLQMSLRLPDTGVYFCARDGGHGFCCSSASCFCGPDVWGQGT 120

Oy 121 TVTVSS 126
Db 121 PVTVSS 126

RESULT 12
Q9ULB4_HUMAN
ID Q9ULB4_HUMAN PRELIMINARY; PRT; 122 AA.
AC Q9ULB4;
RA 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUR=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUR=Primary B-Cells;
RX NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT chains of a human monoclonal antibody with broad reactivity to
RT malignant tumor cells."
RL Nucleic Acids Res. 17:4385-0 (1989).
DR EMBL; BC015760; AAH15760.1; -; mRNA.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR EnsEmbl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
DR Immunoglobulin domain.
KW SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;
SQ
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Best Local Similarity	76.4%	Pred. No. 5.2e-40		
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Db	20	EVQLVESGGGVQPGGSRILRLSCAASGFSFSYAMWVROAPGKLEWVAISGSGGGTYY	79	
Qy	61	ADSVKGRFTISRDNSKNTLYQMNSLRAEDTAVVYCARD-RGIAAGGNYYYIGMDVVRGQG	119	
Db	80	ADSVKGRFTISRDNSRDTLYQMNSLRAEDTAVVYCAKDPRGYSASGN--YTREDYVGGQ	137	
Qy	120	TTVTVSS 126		
Db	138	TLVTVSS 144		
RESULT 14				
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ID	Q6PJ95	HUMAN PRELIMINARY;	PRT;	544 AA.
AC	Q6PJ95			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	IGH1 protein.			
GN	Name=IGH1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22398257; Pubmed=12477932; DOI=10.1073/pnas.242603899;			
RA	Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Tohiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,			
RA	Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Primary B-Cells;			
RG	NTH MGC Project;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBAJ databases.			
DR	EMBL; BC019046; AAH19046.1; -; mRNA.			
DR	HSP; P01863; IADQ.			
DR	SMR; Q6PJ95; 20-473.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003066; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; Cl-set; 3.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 3.			
DR	SMART; SM00406; IGV; 1.			



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:53:15 ; Search time 35 Seconds  
(without alignments)  
297.632 Million cell updates/sec

Title: US-09-920-137f-7  
Perfect score: 668  
Sequence: 1 QVQLVESGGGVQPGSRSLRL.....NYYYGMVDVWGQTTVTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgm2\_6/ptodata/1/iaa/5\_COMB pep.\*  
2: /cgm2\_6/ptodata/1/iaa/6\_COMB pep.\*  
3: /cgm2\_6/ptodata/1/iaa/H\_COMB pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE\_COMB pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572.5	85.7	451	2	US-09-472-087-70
2	565	84.6	126	2	US-09-240-274-26
3	565	84.6	126	2	US-09-848-798-26
4	559	83.7	126	2	US-09-240-274-153
5	559	83.7	126	2	US-09-848-798-153
6	557	83.4	126	2	US-09-240-274-25
7	557	83.4	126	2	US-09-848-798-25
8	554	82.9	310	2	US-09-079-029-11
9	548.5	82.1	125	2	US-09-240-274-140
10	548.5	82.1	125	2	US-09-848-798-140
11	546	81.7	120	2	US-10-330-613A-29
12	541.5	81.1	123	2	US-09-424-840B-6
13	538	80.5	126	2	US-09-240-274-13
14	538	80.5	126	2	US-09-848-798-13
15	537	80.4	124	2	US-09-424-840B-16
16	537	80.4	126	2	US-09-240-274-152
17	537	80.4	126	2	US-09-848-798-152
18	536	80.2	126	2	US-09-240-274-146
19	536	80.2	126	2	US-09-848-798-146
20	535	80.1	126	2	US-09-240-274-17
21	535	80.1	126	2	US-09-848-798-17
22	533	79.8	123	2	US-08-983-607-38
23	530.5	79.4	119	1	US-08-331-398A-46
24	530.5	79.4	119	1	US-08-331-397B-46
25	530.5	79.4	119	1	US-08-759-804A-46
26	530.5	79.4	119	2	US-09-227-693-46
27	530.5	79.4	120	1	US-07-942-245-35

28 529.5 79.3 167 2 US-09-472-087-80 Sequence 80, Appl  
29 529.5 79.3 287 2 US-08-862-124-17 Sequence 17, Appl  
30 529.5 79.3 304 2 US-08-862-124-14 Sequence 14, Appl  
31 526.5 79.1 115 2 US-09-269-332-89 Sequence 89, Appl  
32 526.5 78.8 123 2 US-09-560-198A-2 Sequence 2, Appl  
33 526.5 78.8 127 2 US-09-240-274-139 Sequence 139, Appl  
34 526.5 78.8 127 2 US-09-848-798-139 Sequence 139, Appl  
35 525 78.6 128 2 US-09-840-459-77 Sequence 77, Appl  
36 525 78.6 128 2 US-09-840-459-77 Sequence 77, Appl  
37 525 78.6 128 2 US-09-497-625A-77 Sequence 79, Appl  
38 525 78.6 128 2 US-09-497-625A-79 Sequence 80, Appl  
39 524 78.4 248 2 US-09-315-926A-80 Sequence 145, Appl  
40 522.5 78.2 127 2 US-09-240-274-145 Sequence 145, Appl  
41 522.5 78.2 127 2 US-09-848-798-145 Sequence 145, Appl  
42 522 78.1 126 2 US-09-240-274-16 Sequence 16, Appl  
43 522 78.1 126 2 US-09-848-798-16 Sequence 16, Appl  
44 520 77.8 128 2 US-09-240-274-1 Sequence 1, Appl  
45 520 77.8 128 2 US-09-848-798-1 Sequence 1, Appl

## ALIGNMENTS

## RESULT 1

US-09-472-087-70  
; Sequence 70, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, RILEN B.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-P1  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-70

Query Match 85.7%; Score 572.5; DB 2; Length 451;  
Best Local Similarity 89.8%; Pred. No. 8.1e-49;  
Matches 114; Conservative 1; Mismatches 9; Indels 3; Gaps 2;

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DB 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSVYGHVWVQAPGKLEWVAVIYDGSNKY 60  
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRRAEDTAVYYCARD-RGIAAGGNYYYGMDVWGQ 119  
DB 61 ADSVKGRFTISRDNSKNTLYIQMNSLRRAEDTAVYYCARDPRG--ATLYYYGMDVWGQ 118  
QY 120 TTVTVSS 126  
DB 119 TTVTVSS 125

## RESULT 2

US-09-240-274-26  
; Sequence 26, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

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; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26

Query Match      84.6%; Score 565; DB 2; Length 126;
Best Local Similarity 84.1%; Pred. No. 1e-48;
Matches 106; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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Db 1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVVYDGSNKHY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCARDRGIAAGNNYYGMDVWGPGT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SDSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCARDRGIAAGNNYYGMDVWGPGT 120

QY 121 TTVTVSS 126
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Db 121 TTVTVSS 126

RESULT 3
US-09-848-798-26
; Sequence 26, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-848-798-26

Query Match      84.6%; Score 565; DB 2; Length 126;
Best Local Similarity 84.1%; Pred. No. 1e-48;
Matches 106; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVVYDGSNKHY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCARDRGIAAGNNYYGMDVWGPGT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SDSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCARDRGIAAGNNYYGMDVWGPGT 120

QY 121 TTVTVSS 126
   |||||
Db 121 TTVTVSS 126

RESULT 4
US-09-240-274-153
; Sequence 153, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-153

Query Match      83.7%; Score 559; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 4.1e-48;
Matches 105; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVVYDGSNKHY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCARDRGIAAGNNYYGMDVWGPGT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SDSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCARDRGIAAGNNYYGMDVWGPGT 120

QY 121 TTVTVSS 126
   |||||
Db 121 TTVTVSS 126

RESULT 5
US-09-848-798-153
; Sequence 153, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-848-798-153

Query Match      83.7%; Score 559; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 4.1e-48;
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Db      40 QVQLVQSGGTVVQPGSRSLRLSCAASGTFIFSSYGMHWVRQAPGKGLWVAGIFYDGNKKY 99
Qy      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYIGMDVWGQGT 120
Db      100 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRG-----YYTMDVWGKGT 151
Qy      121 TTVTVSS 126
Db      152 TTVTVSS 157

RESULT 9
US-09-240-274-140
; Sequence 140, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 140
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-140

Query Match      82.1%; Score 548.5; DB 2; Length 125;
Best Local Similarity 83.3%; Pred. No. 4.5e-47;
Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      1 EVQLLESQGGVVQPGSRSLRLSCAASGTFIFSSYGMHWVRQAPGKGLWVALLIYDGNKKEY 60
Qy      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYIGMDVWGQGT 120
Db      61 ADSVKGRFISRDNKNTLYLQVNSLRADDTAVYYCARDQR-AAAGIPYYSRMDVWGQGT 119

Qy      121 TTVTVSS 126
Db      120 TTVTVSS 125

RESULT 10
US-09-848-798-140
; Sequence 140, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; EARLIER FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 140
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-848-798-140

Query Match      82.1%; Score 548.5; DB 2; Length 125;
Best Local Similarity 83.3%; Pred. No. 4.5e-47;
Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      1 EVQLLESQGGVVQPGSRSLRLSCAASGTFIFSSYGMHWVRQAPGKGLWVALLIYDGNKKEY 60
Qy      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYIGMDVWGQGT 120
Db      61 ADSVKGRFISRDNKNTLYLQVNSLRADDTAVYYCARDQR-AAAGIPYYSRMDVWGQGT 119

Qy      121 TTVTVSS 126
Db      120 TTVTVSS 125

RESULT 11
US-10-330-613A-29
; Sequence 29, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-29

Query Match      81.7%; Score 546; DB 2; Length 120;
Best Local Similarity 87.1%; Pred. No. 7.5e-47;
Matches 108; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

Qy      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGKGLWVAVISYDGSNKKY 60
Qy      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYIGMDVWGQGT 120
Db      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR-----SIFGVVIDYGMVWGQGT 116

Qy      121 TTVTV 124
Db      117 TTVTV 120

RESULT 12
US-09-424-840B-6
; Sequence 6, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-848-798-140

Query Match      82.1%; Score 548.5; DB 2; Length 125;
Best Local Similarity 83.3%; Pred. No. 4.5e-47;
Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      1 EVQLLESQGGVVQPGSRSLRLSCAASGTFIFSSYGMHWVRQAPGKGLWVALLIYDGNKKEY 60
Qy      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYIGMDVWGQGT 120
Db      61 ADSVKGRFISRDNKNTLYLQVNSLRADDTAVYYCARDQR-AAAGIPYYSRMDVWGQGT 119

Qy      121 TTVTVSS 126
Db      120 TTVTVSS 125

RESULT 11
US-10-330-613A-29
; Sequence 29, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-29

Query Match      81.7%; Score 546; DB 2; Length 120;
Best Local Similarity 87.1%; Pred. No. 7.5e-47;
Matches 108; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

Qy      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGKGLWVAVISYDGSNKKY 60
Qy      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRGIAAGNYYYIGMDVWGQGT 120
Db      61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR-----SIFGVVIDYGMVWGQGT 116

Qy      121 TTVTV 124
Db      117 TTVTV 120

RESULT 12
US-09-424-840B-6
; Sequence 6, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7

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; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-6

Query Match      81.1%; Score 541.5; DB 2; Length 123;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
Matches 106; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db 1 QVKLESQGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAFMSYDGSNKKY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAAGNYYYYGMDVWGQG 120
Db 61 ADSVKGRFAISRDNKNTLYLQMSLRAEDTAVYYCARDRIAAGNYYYYGMDVWGQG 117

Qy 121 TTVTVSS 126
Db 118 TTVTVSS 123

RESULT 13
US-09-240-274-13
; Sequence 13, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: anti-Rh(D) chain D08
; US-09-240-274-13

Query Match      80.5%; Score 538; DB 2; Length 126;
Best Local Similarity 82.7%; Pred. No. 4.9e-46;
Matches 105; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

Qy 1 QVQLV-ESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKK 59
Db 1 EVQLLESQGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGRGLEWVAFMSYDGSNKK 60

Qy 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAAGNYYYYGMDVWGQG 119
Db 61 YADSVKGRFISRDNKNTLYLQMSLRAEDTAVYYCARDRIAAGNYYYYGMDVWGQG 119

Qy 120 TTVTVSS 126
Db 120 TTVTVSS 126

RESULT 15
US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790338
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-16

Query Match      80.4%; Score 537; DB 2; Length 124;
Best Local Similarity 82.7%; Pred. No. 6.1e-46;
Matches 105; Conservative 6; Mismatches 12; Indels 4; Gaps 2;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db 1 QVKLESQGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGRGLEWVAFMSYDGSNKKY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDRIAAGNYYYYGMDVWGQG 119
Db 61 ADSVKGRFISRDNKNTLYLQMSLRAEDTAVYYCARDRIAAGNYYYYGMDVWGQG 119
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Db      61  ADSVKGRFAISRDRSKNTLYLQMSLRAEDTAVYYCAKD---GRSGSYAREFDGMDVMGQG 117
Qy      120  TTVTVSS 126
Db      118  TTVTVSS 124
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Search completed: December 28, 2005, 14:05:14  
Job time : 36 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	584.5	87.5	123	4	US-10-292-088-117	Sequence 117, Appl
2	584.5	87.5	138	4	US-10-325-694-144	Sequence 144, Appl
3	583	87.3	135	4	US-10-364-743-14	Sequence 14, Appl
4	583	87.3	135	4	US-10-364-743-98	Sequence 98, Appl
5	583	87.3	135	5	US-10-452-593-14	Sequence 14, Appl
6	583	87.3	135	5	US-10-452-593-98	Sequence 98, Appl
7	582	87.1	124	4	US-10-371-942-82	Sequence 82, Appl
8	581.5	87.1	138	4	US-10-325-694-150	Sequence 150, Appl
9	581.5	87.1	457	5	US-10-778-915-1	Sequence 1, Appl
10	581	87.0	126	4	US-10-041-860-17	Sequence 17, Appl
11	581	87.0	126	4	US-10-041-860-209	Sequence 209, Appl
12	581	87.0	126	4	US-10-041-860-282	Sequence 282, Appl
13	581	87.0	126	4	US-10-665-383-14	Sequence 14, Appl
14	580.5	86.9	123	4	US-10-292-088-116	Sequence 116, Appl
15	579	86.7	124	4	US-10-292-088-106	Sequence 106, Appl
16	579	86.7	126	4	US-10-041-860-25	Sequence 25, Appl
17	579	86.7	126	4	US-10-041-860-210	Sequence 210, Appl
18	579	86.7	126	4	US-10-041-860-246	Sequence 246, Appl
19	579	86.7	126	4	US-10-041-860-306	Sequence 306, Appl
20	579	86.7	126	4	US-10-665-383-30	Sequence 30, Appl
21	579	86.7	126	5	US-10-727-155-128	Sequence 128, Appl
22	578.5	86.6	125	4	US-10-292-088-107	Sequence 107, Appl
23	577.5	86.5	123	4	US-10-292-088-115	Sequence 115, Appl
24	577.5	86.5	125	5	US-10-727-155-222	Sequence 222, Appl
25	577	86.4	115	4	US-10-305-347A-7	Sequence 7, Appl
26	577	86.4	115	5	US-10-954-900A-7	Sequence 7, Appl
27	577	86.4	141	5	US-10-858-855-11	Sequence 11, Appl

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; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 138
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-144

Query Match      87.5%; Score 584.5; DB 4; Length 138;
Best Local Similarity 88.2%; Pred. No. 3.5e-48;
Matches 112; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRAQPGNGLEWVAFMSYDGSKKKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRAQPGKLEWVAFISYDGSKKKY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN-YYTYGMDVWGQ 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN-YYTYGMDVWGQ 120

Qy 120 TTTVTSS 126
:|||||:
Db 121 TTTVTSS 127

RESULT 3
US-10-364-743-14
; Sequence 14, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
; NAME/KEY: MISC FEATURE
; LOCATION: (26)-(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-364-743-98

Query Match      87.3%; Score 583; DB 4; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRAQPGNGLEWVAFMSYDGSKKKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYGLHWVRQAPGKLEWVAFISYDGSKKKY 62

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN-YYTYGMDVWGQ 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRVIVPAANKYYYYYYGMVDVWGQ 122

Qy 119 GTT VTSS 126
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Db 123 GTT VTSS 130

RESULT 5
US-10-452-593-14
; Sequence 14, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 135
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; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (26)..(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-452-593-14

Query Match      87.3%; Score 583; DB 5; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFFSSYAMHWVRQAPGNGLEWVAFMSYDGSKKKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLVESGGGVVQPGSRSLRLSCAASGFTFFSSYGLHWVRQAPGKGLWVAFISYDGSKKNY 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN--YYYGMDVWGQ 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVIVPAANKYYYYYGMVWGQ 122
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 GTTVTVSS 126
   :|||||:
Db 123 GTTVTVSS 130
   :|||||:

RESULT 6
US-10-452-593-98
; Sequence 98, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (26)..(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-452-593-98

Query Match      87.3%; Score 583; DB 5; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFFSSYAMHWVRQAPGNGLEWVAFMSYDGSKKKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLVESGGGVVQPGSRSLRLSCAASGFTFFSSYGLHWVRQAPGKGLWVAFISYDGSKKNY 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN--YYYGMDVWGQ 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVIVPAANKYYYYYGMVWGQ 122
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 GTTVTVSS 126
   :|||||:
Db 123 GTTVTVSS 130
   :|||||:
```

```
Db 123 GTTVTVSS 130
   :|||||:

RESULT 7
US-10-371-942-82
; Sequence 82, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-82

Query Match      87.1%; Score 582; DB 4; Length 124;
Best Local Similarity 86.9%; Pred. No. 5.5e-48;
Matches 112; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFFSSYAMHWVRQAPGNGLEWVAFMSYDGSKKKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGGVQPGSRSLRLSCAASGFTFFSSYGMHWVRQAPGKGLWVAVISYDGSKKKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYYGMVWGQT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD--FDYGDYYYYYGMVWGQT 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TVTVSS 126
   :|||||:
Db 119 TVTVSS 124
   :|||||:

RESULT 8
US-10-325-694-150
; Sequence 150, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 138
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-150

Query Match      87.1%; Score 581.5; DB 4; Length 138;
Best Local Similarity 87.4%; Pred. No. 6.8e-48;
Matches 111; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFFSSYAMHWVRQAPGNGLEWVAFMSYDGSKKKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGVVQPGSRSLRLSCAASGFTFFSSYGMHWVRQAPGKGLWVAVISYDGSKKKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN--YYYYGMDVWGQ 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCAKMDMGSGWRPYYYYGMDVWGQ 120
Qy 120 TTVTVSS 126
    |||||
Db 121 TTVTVSS 127
    |||||

RESULT 9
US-10-778-915-1
; Sequence 1, Application US/10778915
; Publication No. US20050180979A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, MALTE
; APPLICANT: LOCHER, MATTHIAS
; APPLICANT: PRANG, NADJA
; APPLICANT: QUADT, CORNELIA
; TITLE OF INVENTION: Anti-EpCAM Immunoglobulins
; FILE REFERENCE: DEBE:031US
; CURRENT APPLICATION NUMBER: US/10/778,915
; CURRENT FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-778-915-1

Query Match 87.1%; Score 581.5; DB 5; Length 457;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
Db 1 EVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCARDRGIAAGN-YYYYGMDVWGQ 119
    |||||
Db 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCAKMDMGSGWRPYYYYGMDVWGQ 120

Qy 120 TTVTVSS 126
    |||||
Db 121 TTVTVSS 127

RESULT 10
US-10-041-860-17
; Sequence 17, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-17
```

```
Query Match 87.0%; Score 581; DB 4; Length 126;
Best Local Similarity 88.1%; Pred. No. 6.9e-48;
Matches 111; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
    |||||
Db 1 QVQLVESGGGVVQPGKSLRLSCAASGTFIFSSYGMHWVRQAPGKLEWVAVIWDGSNKYY 60

Qy 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCARDRGIAAGNYYYYGMDVWGQ 120
    |||||
Db 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCARDQGYRYAGYYIDYGMVWGQ 120

Qy 121 TTVTVSS 126
    |||||
Db 121 TTVTVSS 126

RESULT 11
US-10-041-860-209
; Sequence 209, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-209

Query Match 87.0%; Score 581; DB 4; Length 126;
Best Local Similarity 88.1%; Pred. No. 6.9e-48;
Matches 111; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGTFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
    |||||
Db 1 QVQLVESGGGVVQPGKSLRLSCAASGTFIFSSYGMHWVRQAPGKLEWVAVIWDGSNKYY 60

Qy 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCARDRGIAAGNYYYYGMDVWGQ 120
    |||||
Db 61 ADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVVYCARDQGYRYAGYYIDYGMVWGQ 120

Qy 121 TTVTVSS 126
    |||||
Db 121 TTVTVSS 126

RESULT 12
US-10-041-860-282
; Sequence 282, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
```



## RESULT 14

Query Match	86.78;	Score	579;	DB	4;	Length	124;
Best Local Similarity	88.99;	Pred. No.	1.1e-47;				
Matches	11;	Conservative	2;	Mismatches	10;	Indels	2;
Gaps	1						
Qy	1	QVQLVSGG	GVGVPGR	SLRLSCAASG	FTFSYAMHWYRQAPGNGLEWVA	FMYSYDGSNKYY	60
Db	1	QVQLVSGG	GVGVPGR	SLRLSCAASG	FTFSYGHMHWYRQAPGKLEWVA	VIYSYDGSNKYY	60
Qy	61	ADSVKGRFTIS	RDNISKNTLYLQMN	SLRAEDTAVYYCARD	RGIAGAGNNYYTGM	DVWGQGT	120

Thu Dec 29 10:58:59 2005

Db 61 ADVKGRFTISRDNKNTLYLQWNSLRAEDTAVVYCARGHQLL--GYYYYYGMDVWGQT 118  
Qy 121 TVTVSS 126  
Db 119 TVTVSS 124

Search completed: December 28, 2005, 14:23:02  
Job time : 127.538 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2005, 13:43:04 ; Search time 126.462 Seconds  
(without alignments)  
375.236 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq 21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	98.4	108	5	AAM51165 Anti-tumo
2	559	98.4	108	5	AAM51173 Human Vg/
3	559	98.4	108	5	Aau76334 Human ant
4	559	98.4	108	7	ADJ73533 Erythro
5	559	98.4	108	7	ADJ73534 Erythro
6	559	98.4	108	9	ADW07091 Anti-Psaa
7	559	98.4	129	5	AAM51174 Human rec
8	559	98.4	129	5	AAM51175 Human mAb
9	541	95.2	108	4	AB72884 Human ant
10	541	95.2	108	9	ABE01062 Human IP1
11	541	95.2	109	7	ADP11411
12	541	95.2	215	7	ADP11435
13	540	95.1	128	8	ADM41547
14	540	95.1	130	7	ADD89877 Human ant
15	540	95.1	130	8	ADG64664 Human 9E7
16	540	95.1	130	8	ADG64653 Human ant
17	540	95.1	235	8	ADM41573
18	539	94.9	109	7	ADP11395
19	539	94.9	215	7	ADP11419
20	538	94.7	108	8	ADS19298
21	536	94.4	108	9	ADW08866 Light cha
22	535	94.2	108	8	ADW08866 IGF-IR an
23	534	94.0	108	8	AD122138 Anti-plat
24	534	94.0	109	7	ABE01057 Human IP1
					ADP11403 2D8 anti-

25	534	94.0	109	7	ADP11415	Adf11415 9H7 anti-
26	534	94.0	215	7	ADP11439	Adf11439 9H7 anti-
27	534	94.0	215	7	ADP11427	Adf11427 2D8 anti-
28	531.5	93.6	129	6	ABP57362	Abp57362 Anti-TRAI
29	529.5	93.2	107	6	ABR54916	ABr54916 Light cha
30	529.5	93.2	107	9	ABE19292	ABe19292 Igg Kappa
31	529.5	93.2	236	9	AD251040	Ad251040 Amino aci
32	529	93.1	128	7	ADJ73528	Adj73528 Erythro
33	529	93.1	251	5	ABP45038	ABp45038 Human Bly
34	529	93.1	251	7	ADG95865	ADg95865 Single ch
35	528.5	93.0	129	7	ADJ73532	Adj73532 Erythro
36	525	92.4	109	4	AB62756	AB62756 Human HIV
37	524.5	92.3	107	9	ADY26776	Ady26776 Anti-NGF-
38	524.5	92.3	110	9	ADX02205	Adx02205 SARS coro
39	524.5	92.3	110	9	ADX02049	Adx02049 SARS coro
40	524.5	92.3	214	8	ADH34591	ADh34591 023 light
41	524.5	92.3	251	9	ADX01956	ADx01956 SARS coro
42	524.5	92.3	252	9	ADX02034	ADx02034 SARS coro
43	524	92.3	108	9	ADW08864	ADw08864 IGF-IR an
44	524	92.3	108	9	ABE01064	ABe01064 Human IP1
45	523.5	92.2	224	4	AB999371	AB999371 Human int

#### ALIGNMENTS

##### RESULT 1

AAM51165  
ID AAM51165 standard; protein; 108 AA.

AC AAM51165;

XX 10-JUN-2002 (first entry)

DE Anti-tumour necrosis factor antibody light chain variable region.

KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antidiabetic; antiallergic; antinflammatory; antiscoking;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antiangiinal; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy.

XX Homo sapiens.

Key	Region	Location/Qualifiers
FT	Region	1..23 /label= FR1
FT	Region	24..34 /label= CDR1
FT	Region	35..49 /label= FR2
FT	Region	50..56 /label= CDR2
FT	Region	57..88 /label= FR3
FT	Region	89..98 /label= CDR3
FT	Region	99..108 /label= J6
XX		WO200212502-A2.
XX		14-FEB-2002.
XX		07-AUG-2001; 2001WO-US024785.
XX		07-AUG-2000; 2000US-0223360P.
XX		29-SEP-2000; 2000US-0236826P.
XX		01-AUG-2001; 2001US-00920137.
XX		(CENZ ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
 PI WPT; 2002-217194/27.  
 DR  
 XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 PT angina pectoris, myocardial infarction, leprosy.  
 PS  
 XX Claim 9; Page 129-130; 131pp; English.  
 XX  
 CC The present sequence is that of the light chain variable region of an  
 CC anti-tumor necrosis factor (TNF) antibody of the invention. The  
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
 CC humanised and/or complementarity determining region (CDR)-grafted anti-  
 CC TNF antibodies, immunoglobulins, cleavage products and other specified  
 CC portions and variants, as well as anti-TNF antibody compositions,  
 CC encoding or complementary nucleic acids, vectors, host cells,  
 CC plants, and methods of making and using them. The anti-TNF antibody  
 CC comprises at least a portion of an immunoglobulin molecule, especially  
 CC the heavy chain and/or light chain variable regions given in AAM51164 and  
 CC in the present sequence, or either all of the CDRs of the heavy chain  
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
 CC 63). The antibody may inhibit TNF-induced cell adhesion molecules,  
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. It is useful for diagnosing or treating a TNF related  
 CC condition in a cell, tissue, organ or animal (claimed) such as rheumatoid  
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,  
 CC sickle cell anaemia, diabetes, a cardiovascular disease such as  
 CC atherosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
 CC Creutzfeldt-Jakob disease  
 XX  
 XX Sequence 108 AA;  
 SQ  
 Query Match 98.4%; Score 559; DB 5; Length 108;  
 Best Local Similarity 99.1%; Pred. NO. 1.1e-37;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
 QY 61 RFSGSGGTDTLTLSLEPEDFAVYVYQQRSNPPFTFGTGKVDIK 108  
 DB 61 RFSGSGGTDTLTLSLEPEDFAVYVYQQRSNPPFTFGTGKVDIK 108  
 RESULT 2  
 AAM51173  
 ID AAM51173 standard; protein; 108 AA.  
 AC AAM51173;  
 XX  
 XX 10-JUN-2002 (first entry)  
 DT  
 XX Human Vg/38k-type light chain variable region.  
 DE  
 XX Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;  
 KW complementarity determining region; antirheumatic; antiarthritic;  
 KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antischlicking;  
 KW antiangiogenic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
 KW antiangiatic; cardiant; antibacterial; virucide; fungicide; antileprotic;  
 KW protozoacide; cycostatic; neuroprotective; antiparkinsonian; nootropic;  
 KW human; diagnosis; therapy; Vg/38k.  
 XX  
 XX Homo sapiens.  
 OS  
 XX

PH Key Location/Qualifiers  
 FT Region 1. .23  
 FT /label= FR1  
 FT Region 24. .34  
 FT /label= CDR1  
 FT Region 35. .49  
 FT /label= FR2  
 FT Region 50. .56  
 FT /label= CDR2  
 FT Region 57. .88  
 FT /label= FR3  
 FT Region 89. .98  
 FT /label= CDR3  
 FT Region 99. .108  
 FT /label= J3  
 XX WO200212502-A2.  
 FN 14-FEB-2002.  
 PD 07-AUG-2001; 2001WO-US024785.  
 XX 07-AUG-2000; 2000US-0223360P.  
 PR 29-SEP-2000; 2000US-0236826P.  
 PR 01-AUG-2001; 2001US-00920137.  
 XX (CENZ ) CENTOCOR INC.  
 PA Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
 XX WPT; 2002-217194/27.  
 XX N-PSDB; ABL53513.  
 DR Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 XX angina pectoris, myocardial infarction, leprosy.  
 XX  
 XX Example 3; Fig 5; 131pp; English.  
 PS  
 CC The present sequence is that of a human Vg/38k-type light chain variable  
 CC region encoded by a human germline gene in a transgenic mouse used in  
 CC human monoclonal antibody (mAb) construction. A GENTRV fusion was  
 CC performed using spleen cells from a hybrid mouse containing human  
 CC variable and constant region antibody transgenes that was immunised with  
 CC recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were  
 CC obtained that bound immobilised human TNF alpha with apparently high  
 CC avidity. These mAbs had a totally human IgG1, kappa isotype. The mature  
 CC portion of the light chain variable region of 2 of the mAbs, TNV14 and  
 CC TNV15, were identical (see AAM51174) to the present sequence, while the  
 CC light chain variable region of 2 others, TNV148(B) and TNV196 (see  
 CC AAM51175), differed by a single amino acid residue. The invention  
 CC provides human, primate, rodent, mammalian, chimeric, humanised and/or  
 CC complementarity determining region (CDR)-grafted anti-TNF antibodies, and  
 CC immunoglobulins, and cleavage products and variants, as well as anti-TNF  
 CC antibody compositions, encoding or complementary nucleic acids, vectors,  
 CC host cells, compositions, formulations, devices, transgenic animals,  
 CC transgenic plants, and methods of making and using them. The anti-TNF  
 CC antibody comprises at least a portion of an immunoglobulin molecule,  
 CC especially the heavy chain and/or light chain variable regions given in  
 CC the present sequence and in AAM51165, or either all of the CDRs of the  
 CC heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see  
 CC AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion  
 CC molecules, inhibit TNF binding to receptor, or provide Arthritic Index  
 CC improvement in a mouse model. They are useful for diagnosing or treating  
 CC a TNF related condition in a cell, tissue, organ or animal (claimed) such  
 CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,  
 CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular  
 CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina  
 CC pectoris or myocardial infarction, an infectious disease in a cell such  
 CC as bacterial, viral, and fungal infections, pneumonia, leprosy and  
 CC malaria, a malignant disease such as leukaemia, chronic myelocytic  
 CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological  
 CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,  
 CC

CC Alzheimer's disease and Creutzfeldt-Jakob disease  
 XX Sequence 108 AA;  
 SQ

Query Match 98.4%; Score 559; DB 5; Length 108;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-37;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTDFTLTISLSLEPEDFAVYICQQRSNWPPFTFGPTKVDIK 108  
 DB 61 RFSGSGSGTDFTLTISLSLEPEDFAVYICQQRSNWPPFTFGPTKVDIK 108

RESULT 3  
 AAU76334  
 ID AAU76334 standard; peptide; 108 AA.  
 XX AC AAU76334;  
 XX DT 21-MAY-2002 (first entry)  
 XX DE Human anti-dual integrin antibody complete variable region #2.  
 XX Human; antibody; dual integrin; HC CDR; variable region; LC CDR;  
 KW medical device; immune related disease; rheumatoid arthritis;  
 KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;  
 KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;  
 KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;  
 KW infectious disease; pneumonia; leprosy; malaria; malignant disease;  
 KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;  
 KW neurological disease; multiple sclerosis; Parkinson's disease;  
 KW Alzheimer's disease; Creutzfeldt-Jakob disease.  
 XX Homo sapiens.  
 XX WO200212501-A2.  
 XX 14-FEB-2002.  
 XX 07-AUG-2001; 2001WO-US024784.  
 XX 07-AUG-2000; 2000US-0223363P.  
 XX 01-AUG-2001; 2001US-00920267.  
 XX (CENZ ) CENTOCOR INC.  
 XX Giles-Komar J, Heavner G, Snyder L, Trikha M;  
 XX WPI; 2002-217193/27.  
 XX Novel isolated mammalian anti-dual integrin antibody, useful for  
 PT diagnosing or treating dual integrin related condition such as rheumatoid  
 PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.  
 XX Claim 1; Page 134; 144pp; English.

CC The invention relates to an isolated mammalian anti-dual integrin  
 CC antibody having at least one of the human heavy chain or light chain  
 CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also  
 CC included are the nucleic acids encoding the CDRs, a vector comprising the  
 CC nucleic acids, a host cell comprising the vector, an anti-idiotypic  
 CC antibody that binds to the anti-dual integrin, a medical device comprising  
 CC the antibody suitable for administration by parenteral, subcutaneous,  
 CC intramuscular, intravenous, intrarticular, intrabronchial,  
 CC intradominal, intracapsular, intracartilaginous, intracavitary,  
 CC intracerebellar, or other routes as given in specification. The antibody  
 CC is useful for diagnosing or treating a dual integrin related condition in  
 CC an animal for example, immune related disease such as rheumatoid  
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,

CC sickle cell anaemia, diabetes, cardiovascular disease such as  
 CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,  
 CC myocardial infarction, infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma, multiple myeloma; neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,  
 CC Creutzfeldt-Jakob disease and many other diseases given in the  
 CC specification. The present sequence is an anti-dual integrin human  
 CC variable region containing at least one of the six CDRs listed above  
 CC (AAU76327-AAU76332)  
 XX SQ Sequence 108 AA;  
 Query Match 98.4%; Score 559; DB 5; Length 108;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-37;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTDFTLTISLSLEPEDFAVYICQQRSNWPPFTFGPTKVDIK 108  
 DB 61 RFSGSGSGTDFTLTISLSLEPEDFAVYICQQRSNWPPFTFGPTKVDIK 108

RESULT 4  
 ADJ73533  
 ID ADJ73533 standard; protein; 108 AA.  
 XX AC ADJ73533;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Erythropoietin light chain mimetibody SeqID 989.  
 XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;  
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;  
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;  
 KW erythropoietin.  
 XX Synthetic.  
 XX WO2003084477-A2.  
 XX 16-OCT-2003.  
 XX 24-MAR-2003; 2003WO-US009139.  
 XX 29-MAR-2002; 2002US-0368791P.  
 XX (CENZ ) CENTOCOR INC.  
 XX Heavner GA, Knight DM, Scallion BJ, Ghayeb J;  
 XX WPI; 2003-804237/75.  
 XX New CDR mimetibody comprising a portion of a heavy or light chain  
 PT variable region comprising human framework or ligand binding region,  
 PT useful for preparing a composition for treating e.g., immune,  
 PT cardiovascular or neurologic disease.  
 XX Example 2; SEQ ID NO 989; 97pp; English.  
 CC This invention relates to novel mammalian CDR mimetibodies, specific  
 CC portions or variants thereof. Specifically, it refers to an antibody  
 CC fragment where a protein has been inserted into, or replaces a portion  
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at  
 CC least one portion of a heavy chain or light chain variable region, which  
 CC itself comprises at least one human framework region and at least one  
 CC ligand binding region (LBR). The present invention describes human  
 CC mimetibodies, including modified immunoglobulins and cleavage products



CC composition are useful for treating or preventing an individual suffering  
 CC from disorders or diseases associated with S. pneumoniae, e.g. pneumonia,  
 CC meningitis and/or sepsis. This is the amino acid sequence of anti-  
 CC pneumococcal surface adhesin A (PsaA)-antibody 9A7 kappa light chain  
 CC variable region.  
 XX  
 SQ Sequence 108 AA;

Query Match 98.4%; Score 559; DB 9; Length 108;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-37;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIYDASNRATGIPA 60

Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIYDASNRATGIPA 60

Oy 61 RFGSGSGTDTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108

Db 61 RFGSGSGTDTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108

RESULT 7  
 AAM51174

ID AAM51174 standard; protein; 129 AA.

XX AC AAM51174;

XX DT 10-JUN-2002 (first entry)

XX DE Human recombinant mAb TNV14, TNV15 light chain variable region.

XX KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
 KW complementarity determining region; antirheumatic; antiarthritis;  
 KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antischlicking;  
 KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
 KW antiangiatic; cardiact; antibacterial; virucide; fungicide; antileptotic;  
 KW protozoacide; cycostatic; neuroprotective; antiparkinsonian; nootropic;  
 KW human; diagnosis; therapy; TNV14; TNV15; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT Protein /label= Signal\_peptide  
 FT /label= Mature\_protein  
 FT Region 21..43  
 FT /label= FR1  
 FT Region 44..54  
 FT /label= CDR1  
 FT Region 55..69  
 FT /label= FR2  
 FT Region 70..76  
 FT /label= CDR2  
 FT Region 77..108  
 FT /label= FR3  
 FT Region 109..118  
 FT /label= CDR3  
 FT Region 119..129  
 FT /label= J3

XX WO200212502-A2.

XX PD 14-FEB-2002.

XX PF 07-AUG-2001; 2001WO-US024785.

XX PR 07-AUG-2000; 2000US-0223360P.

XX PR 29-SEP-2000; 2000US-0236826P.

XX PR 01-AUG-2001; 2001US-00920137.

XX PA (CENZ ) CENTOCOR INC.

XX

PI Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
 DR WPI; 2002-217194/27.  
 DR N-PSDB; ABL53514.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
 PT angina pectoris, myocardial infarction, leprosy.

XX Example 3; Fig 5; 131pp; English.

XX The present sequence is that of the light chain variable region of anti-  
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibodies  
 CC (mAbs) TNV14 and TNV15. These are human mAbs produced from a GenTIV  
 CC fusion using spleen cells from a hybrid mouse containing human variable  
 CC and constant region antibody transgenes that was immunised with human TNF  
 CC and have a totally human IgG1, kappa isotype. The mature portion of the  
 CC light chain variable region is identical to that of the Vg/38-type light  
 CC chain germline sequence (see AAM51173). The light chain variable regions  
 CC of 2 other human mAbs (see AAM51175) show a single amino acid difference.  
 CC The invention provides human, primate, mammalian, rodent, chimeric,  
 CC TNF antibodies and/or complementarity determining region (CDR)-grafted anti-  
 CC TNF antibodies, immunoglobulins, cleavage products and other specified  
 CC portions and variants, as well as anti-TNF antibody compositions,  
 CC encoding or complementary nucleic acids, vectors, host cells,  
 CC compositions, formulations, devices, transgenic animals, transgenic  
 CC plants, and methods of making and using them. The anti-TNF antibody  
 CC comprises at least a portion of an immunoglobulin molecule, especially  
 CC the heavy chain and/or light chain variable regions given in the present  
 CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. They are useful for diagnosing or treating a TNF  
 CC related condition in a cell, tissue, organ or animal (claimed) such as  
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
 CC Creutzfeldt-Jakob disease

XX SQ Sequence 129 AA;

Query Match 98.4%; Score 559; DB 5; Length 129;  
 Best Local Similarity 99.1%; Pred. No. 1.3e-37;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIYDASNRATGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIYDASNRATGIPA 80

Oy 61 RFGSGSGTDTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108

Db 81 RFGSGSGTDTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 128

RESULT 8  
 AAM51175

ID AAM51175 standard; protein; 129 AA.

XX AC AAM51175;

XX DT 10-JUN-2002 (first entry)

XX DE Human mAb TNV14(B), TNV196 light chain variable region.

XX KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
 KW complementarity determining region; antirheumatic; antiarthritis;

XX

antitumor; antiasthmatic; antiallergic; antiinflammatory; antisickling; antiadrenergic; antiarteriosclerotic; antiatherosclerotic; vasotropic; antiangiogenic; cardiac; antibacterial; virocidic; fungicide; antileprotic; protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic; human; diagnosis; therapy; TNV148(B); TNV196; monoclonal antibody; mAb.

Homo sapiens.

Location/Qualifiers

1. .20 /label= Signal\_peptide

20. .129 /label= Mature\_protein

21. .43 /label= FR1

44. .54 /label= CDR1

55. .69 /label= FR2

70. .76 /label= CDR2

77. .108 /label= FR3

109. .118 /label= CDR3

119. .129 /label= J3

WO200212502-A2.

14-FEB-2002.

07-AUG-2001; 2001WO-US024785.

07-AUG-2000; 2000US-0223360P.

29-SEP-2000; 2000US-0236826P.

01-AUG-2001; 2001US-00920137.

(CENZ ) CENTOCOR INC.

Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;

WPI; 2002-217194/27.

N-PSDB; ABL53515.

Novel isolated mammalian anti-tumor necrosis factor antibody, useful for treating sickle cell anemia, diabetes, atherosclerosis, restenosis, angina pectoris, myocardial infarction, leprosy.

Example 3; Fig 5; 131pp; English.

The present sequence is that of the light chain variable region of anti-tumour necrosis factor (TNF) human recombinant monoclonal antibodies (mAbs) TNV148(B) and TNV196. These are human mAbs produced from a GenTmV fusion using spleen cells from a hybrid mouse containing human variable and constant region antibody transgenes that was immunised with human TNF alpha. The human mAbs bind immobilised human TNF alpha with high avidity and have a totally human IgG1, kappa isotype. The mature portion of the light chain variable region differs from that of the Vg/38-type light chain germline sequence (see AAM51173) by a single residue (Tyr-50 replacing Ser). The light chain variable regions of 2 other human mAbs (see AAM51174) were identical to the germline sequence. The invention provides isolated human, primate, rodent, mammalian, chimeric, humanised and/or complementarity determining region (CDR)-grafted anti-TNF antibodies, immunoglobulins, cleavage products and other specified portions and variants, as well as anti-TNF antibody compositions, encoding or complementary nucleic acids, vectors, host cells, compositions, formulations, devices, transgenic animals, transgenic plants, and methods of making and using them. The anti-TNF antibody comprises at least a portion of an immunoglobulin molecule, especially the heavy chain and/or light chain variable regions given in the present sequence and in AAM51165, or either all of the CDRs of the heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-

63). The antibodies may inhibit TNF-induced cell adhesion molecules, inhibit TNF binding to receptor, or provide Arthritic Index improvement in a mouse model. They are useful for diagnosing or treating a TNF related condition in a cell, tissue, organ or animal (claimed) such as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular disease such as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or myocardial infarction, an infectious disease in a cell such as bacterial, viral, and fungal infections, pneumonia, leprosy and malaria, a malignant disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological disease such as multiple sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-Jakob disease

Sequence 129 AA;

Query Match 98.4%; Score 559; DB 5; Length 129;  
Best Local Similarity 99.1%; Pred. No. 1.3e-37;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 80  
Qy 61 RFGSGSGTDFTLTITISLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108  
Db 81 RFGSGSGTDFTLTITISLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 128

RESULT 9

AAB72884

ID AAB72884 standard; protein; 108 AA.

AC AAB72884;

XX 10-MAY-2001 (first entry)

XX Human anti-HER2/neu antibody 2-E8 light chain.

XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;

XX 1-D2; 2-E8; growth factor receptor.

XX Homo sapiens.

XX WO200109187-A2.

XX 08-FEB-2001.

XX 25-JUL-2000; 2000WO-US020272.

XX 29-JUL-1999; 99US-0146313P.

XX 10-MAR-2000; 2000US-0188539P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Deo Y;

XX WPI; 2001-168698/17.

XX N-PSDB; AAF75590.

New human monoclonal antibody that specifically binds to growth factor receptor HER2/neu, for treating, preventing or diagnosing diseases characterized by aberrant HER2/neu expression e.g. cancers.

Disclosure; Page 110; 113pp; English.

The present invention provides the protein and coding sequences for human monoclonal antibodies which bind specifically to the HER2/neu growth factor receptor (also known as erbB2). These are designated 3-F2, 1-D2 and 2-E8. They can be used in the immunotherapy-based treatment and prognosis of cancers, particularly adenocarcinomas such as salivary gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas, and ovarian cancer. The present sequence is part of an antibody of the



CC invention  
 XX Sequence 108 AA;  
 SQ

Query Match 95.2%; Score 541; DB 4; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 3e-36;  
 Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
 |||||  
 Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
 |||||

Qy 61 RFSGSGSTDTLTLSLEPEDFAVYQCQRSNWPPFTFGPCTKVDIK 108  
 |||||  
 Db 61 RFSGSGSTDTLTLSLEPEDFAVYQCQRSNWPPFTFGPCTKVDIK 108  
 |||||

RESULT 10  
 AEB01062  
 ID AEB01062 standard; protein; 108 AA.  
 AC AEB01062;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX Human IP10 antibody light chain variable region, SEQ ID NO 90.  
 DE antibody; IP-10; inflammation; immune disorder; dermatological disease;  
 KW respiratory disease; neurological disease; degeneration; infection;  
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;  
 KW Gastrointestinal-Gen.; Antitumor; Dermatological; Immunosuppressive;  
 KW Antidiabetic; Antiproliferative; Antithyroid; Antistomatitis;  
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;  
 KW Antiparkinsonian; Antiangiogenic; Antiartherosclerotic; Virucide;  
 KW Antibacterial; light chain variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2005058815-A2.  
 XX  
 XX 30-JUN-2005.  
 XX  
 XX 10-DEC-2004; 2004WO-US041506.  
 XX  
 XX 10-DEC-2003; 2003US-0529180P.  
 XX  
 XX (MEDA-) MEDAREX INC.  
 XX  
 XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;  
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;  
 XX  
 XX WPI; 2005-467095/47.  
 XX  
 XX N-PSDB; AEB01088.  
 XX  
 XX Isolated human monoclonal antibody or an antigen-binding portion, which  
 PT specifically binds to human interferon gamma inducible protein 10 (IP-  
 PT 10), useful for treating viral or bacterial infection, or inflammatory or  
 PT autoimmune diseases.  
 XX  
 XX Claim 35; SEQ ID NO 90; 179pp; English.  
 XX  
 XX The invention relates to an isolated human monoclonal antibody or an  
 CC antigen-binding portion, which specifically binds to human IP-10 and  
 CC exhibits at least one property selected from: inhibits binding of IP-10  
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced  
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-  
 CC react with mouse IP-10; does not cross-react with human MIG; or does not  
 CC cross-react with human ITAC. The isolated human monoclonal antibody is  
 CC useful for treating an inflammatory or autoimmune disease including  
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease  
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus  
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,  
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'

CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary  
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,  
 CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,  
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative  
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,  
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory  
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative  
 CC glomerulonephritis, rapidly progressive glomerulonephritis), or  
 CC atherosclerosis. It is also useful for treating a viral or bacterial  
 CC infection involving unwanted IP-10 activity in a subject, where the viral  
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present  
 CC sequence represents the amino acid sequence of a human IP10 monoclonal  
 CC antibody light chain variable region.  
 XX  
 XX Sequence 108 AA;  
 SQ

Query Match 95.2%; Score 541; DB 9; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 3e-36;  
 Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
 |||||  
 Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
 |||||

Qy 61 RFSGSGSTDTLTLSLEPEDFAVYQCQRSNWPPFTFGPCTKVDIK 108  
 |||||  
 Db 61 RFSGSGSTDTLTLSLEPEDFAVYQCQRSNWPPFTFGPCTKVDIK 108  
 |||||

RESULT 11  
 ADF11411  
 ID ADF11411 standard; protein; 109 AA.  
 AC ADF11411;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 XX 16E1 anti-OPGL antibody kappa chain variable region SEQ ID NO:24.  
 DE human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;  
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003086289-A2.  
 XX  
 XX 23-OCT-2003.  
 XX  
 XX 07-APR-2003; 2003WO-US010749.  
 XX  
 XX 05-APR-2002; 2002US-0370407P.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Boyle WJ, Medlock B, Sullivan JK, Elliott RL, Martin F, Huang H;  
 PI WPI; 2003-845253/78.  
 XX  
 XX N-PSDB; ADF11410.  
 XX  
 XX New isolated antibody that specifically binds osteoprotegerin ligand,  
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,  
 PT bone loss from arthritis, Paget's disease or osteopenia.  
 XX  
 XX Claim 6; SEQ ID NO 24; 156pp; English.  
 XX  
 XX The present invention describes an isolated human antibody (I) that  
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
 CC pharmaceutical composition comprising a pharmaceutical carrier and a  
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder  
 CC in a patient, comprising administering to a patient the pharmaceutical  
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method  
 CC for detecting OPGL in a biological sample, comprising contacting the

CC sample with (1) under conditions that allow for binding of the antibody  
 CC to OPGL, and measuring the level of bound antibody in the sample. (1) has  
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in  
 CC gene therapy. The composition and methods are useful in diagnosing or  
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,  
 CC Paget's disease or osteopenia. The antibody (1) may also be used for  
 CC detecting OPGL in biological samples and in identifying cells or tissues  
 CC that produce the protein. The present sequence represents a sequence  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 109 AA;

Query Match 95.2%; Score 541; DB 7; Length 109;  
 Best Local Similarity 95.4%; Pred. No. 3.1e-36;  
 Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWSYQKPGQAPRLIYDASNRATGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWSYQKPGQAPRLIYDASNRATGIPA 60  
 QY 61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPPTFGGTVKDIK 108  
 DB 61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPPTFGGTVKLEIK 108

RESULT 12  
 ADF11435  
 ID ADF11435 standard; protein; 215 AA.  
 XX  
 AC ADF11435;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE 16E1 anti-OPGL antibody light chain SEQ ID NO:48.  
 XX  
 KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;  
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003086289-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 07-APR-2003; 2003WO-US010749.  
 XX  
 PR 05-APR-2002; 2002US-0370407P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;  
 XX  
 DR WPI; 2003-845253/78.  
 DR N-PSDB; ADF11434.  
 XX  
 FT New isolated antibody that specifically binds osteoprotegerin ligand,  
 FT useful for diagnosing or treating bone disorders, such as osteoporosis,  
 FT bone loss from arthritis, Paget's disease or osteopenia.  
 XX  
 PS Claim 16; SEQ ID NO 48; 156pp; English.

CC The present invention describes an isolated human antibody (1) that  
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
 CC pharmaceutical composition comprising a pharmaceutical carrier and a  
 CC therapeutic amount of (1); (2) methods of treating an osteopenic disorder  
 CC in a patient, comprising administering to a patient the pharmaceutical  
 CC composition of (1) or a pharmaceutical amount of (1); and (3) a method  
 CC for detecting OPGL in a biological sample, comprising contacting the  
 CC sample with (1) under conditions that allow for binding of the antibody  
 CC to OPGL, and measuring the level of bound antibody in the sample. (1) has  
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in  
 CC gene therapy. The composition and methods are useful in diagnosing or

CC treating bone disorders, such as osteoporosis, bone loss from arthritis,  
 CC Paget's disease or osteopenia. The antibody (1) may also be used for  
 CC detecting OPGL in biological samples and in identifying cells or tissues  
 CC that produce the protein. The present sequence represents a sequence  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 215 AA;

Query Match 95.2%; Score 541; DB 7; Length 215;  
 Best Local Similarity 95.4%; Pred. No. 5.8e-36;  
 Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWSYQKPGQAPRLIYDASNRATGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWSYQKPGQAPRLIYDASNRATGIPA 60  
 QY 61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPPTFGGTVKDIK 108  
 DB 61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPPTFGGTVKLEIK 108

RESULT 13  
 ADM41547  
 ID ADM41547 standard; protein; 128 AA.  
 XX  
 AC ADM41547;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.  
 XX  
 KW Human; monoclonal antibody; antibody; interleukin-1; receptor;  
 KW antiasthmatic; antiinflammatory; dermatological; antiallergic;  
 KW protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;  
 KW analgesic; antidiabetic; nephrotropic; antianemic; nootropic;  
 KW anticonvulsant; dermatological; antigout; antiparkinsonian; antidiabetic;  
 KW cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004022718-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 05-SEP-2003; 2003WO-US027978.  
 XX  
 PR 06-SEP-2002; 2002US-0408719P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;  
 PI Elliott G;  
 XX  
 DR WPI; 2004-248462/23.  
 DR N-PSDB; ADM41546.  
 XX  
 FT Isolated human antibody that specifically binds interleukin-1 receptor  
 FT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as  
 FT rheumatoid arthritis, osteoarthritis and inflammatory conditions.  
 XX  
 PS Claim 2; SEQ ID NO 12; 179pp; English.

CC The present sequence is that of human anti-interleukin-1 receptor type 1  
 CC (IL-1R1) monoclonal antibody (Mab) 26F5 kappa chain variable region.  
 CC Human Mabs to IL-1R1 were prepared using the Hco7 strain of transgenic  
 CC mice, which expresses human antibody genes. These mice were immunised  
 CC with purified recombinant IL-1R1, and splenocytes from immunised mice  
 CC were fused to a mouse myeloma cell line to generate hybridomas.  
 CC Hybridomas which secreted a Mab that bound with high avidity to IL-1R1  
 CC were selected. The Mabs inhibit IL-1 signalling by competing with IL-1  
 CC beta and IL-1alpha binding to IL-1R. These Mabs, as well as single chain  
 CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies  
 CC and (Fab')2 antibodies derived from them, are used in methods of treating

CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.  
 CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral  
 CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,  
 CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,  
 CC Clostridium associated illnesses, coronary conditions, cancer including  
 CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,  
 CC fibromyalgia, glomerulonephritis, graft versus host disease,  
 CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,  
 CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,  
 CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,  
 CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,  
 CC septic shock, side effects of radiation therapy, temporal mandibular  
 CC joint disease, sleep disturbance, uveitis, or an inflammatory condition  
 CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic  
 CC surgery, infection or other disease processes.  
 XX  
 SQ Sequence 128 AA;

Query Match 95.1%; Score 540; DB 8; Length 128;  
 Best Local Similarity 96.3%; Pred. No. 4.3e-36;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60  
 DB 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 80  
 QY 61 RFGSGSGTDFTLTISLSEPEDEFAVYQCQRSNWPPFTFGCTKVDIK 108  
 DB 81 RFGSGSGTDFTLTISLSEPEDEFAVYQCQRSNWPPFTFGGTRKVEIK 128

## RESULT 14

ADD89877  
 ID ADD89877 standard; protein; 130 AA.

XX  
 AC ADD89877;

XX 29-JAN-2004 (first entry)

XX Human anti-TNF antibody 9E7 light chain variable region.

DE Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;  
 KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;  
 KW neuroprotective.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 44..54

FT /note= "CDR1"

FT Region 65..71

FT /note= "CDR2"

FT Region 109..118

FT /note= "CDR3"

XX WO2003083061-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009072.

XX 26-MAR-2002; 2002US-0367903P.

XX (CENZ ) CENTOCOR INC.

XX Giles-Komar J, Scallion BJ, Carton JM;

XX WPI; 2003-804040/75.

XX N-PSDB; ADD89883.

XX New isolated mammalian anti-tumour necrosis factor (TNF) antibody, useful  
 PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,  
 PT anorexia, cachexia, or bacterial infection.

XX Claim 1; Fig 3B; 87pp; English.  
 PS

XX The present sequence is that of the light chain variable region of human  
 CC anti-tumour necrosis factor (TNF) monoclonal antibody 9E7. This human TNF  
 CC reactive IgG monoclonal antibody was generated by cloning variable and  
 CC constant region DNA in vector pC4 and expression in CHO cells. The  
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
 CC humanized and/or CDR-grafted anti-TNF antibodies, immunoglobulins, their  
 CC cleavage products, other specified portions and variants, as well as anti  
 CC -TNF antibody compositions, nucleic acids encoding these, vectors, host  
 CC cells, methods for producing the antibodies using a host cell, transgenic  
 CC animal or transgenic plant or plant cell, and therapeutic compositions  
 CC methods and devices. The antibody, nucleic acid, protein, composition and  
 CC methods are useful for diagnosing or treating an anti-TNF related  
 CC condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular,  
 CC infectious, and/or neurological disease.

XX Sequence 130 AA;

Query Match 95.1%; Score 540; DB 7; Length 130;  
 Best Local Similarity 96.3%; Pred. No. 4.3e-36;

Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60  
 DB 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 80  
 QY 61 RFGSGSGTDFTLTISLSEPEDEFAVYQCQRSNWPPFTFGCTKVDIK 108  
 DB 81 RFGSGSGTDFTLTISLSEPEDEFAVYQCQRSNWPPFTFGGTRKVEIK 128

## RESULT 15

ADS64664  
 ID ADS64664 standard; protein; 130 AA.

XX  
 AC ADS64664;

XX 16-DEC-2004 (first entry)

XX Human 9E7LC light chain protein.

DE Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;  
 KW obesity; immune related disease; rheumatoid arthritis;  
 KW cardiovascular disease; stroke; malignant disease; leukaemia;  
 KW neurological disease; multiple sclerosis; infection; hepatitis;  
 KW anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;  
 KW neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;  
 KW human; 9E7LC; light chain.

XX Homo sapiens.

XX US2004185047-A1.

XX 23-SEP-2004.

XX 21-MAR-2003; 2003US-00394471.

XX 21-MAR-2003; 2003US-00394471.

XX (GILE/) GILES-KOMAR J.

XX (SCAL/) SCALLON B J.

XX (CART/) CARTON J M.

XX Giles-Komar J, Scallion BJ, Carton JM;

XX WPI; 2004-676151/66.

XX N-PSDB; ADS64661.

XX Novel isolated mammalian anti-tumour necrosis factor (TNF) alpha antibody  
 PT capable of inhibiting binding of TNF alpha to TNF receptor, useful for  
 PT treating TNF-related diseases such as obesity or rheumatoid arthritis.

```

XX Example 4; Fig 3; 45pp; English.
PS
XX
CC The present invention relates to a mammalian anti-tumour necrosis factor
CC (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
CC receptor. The invention is useful for diagnosing or treating an anti-TNF
CC related condition in a cell, tissue, organ or animal and in
CC immunotherapy. The invention is also useful for treating TNF related
CC diseases chosen from obesity, immune related disease such as rheumatoid
CC arthritis, cardiovascular disease such as stroke, malignant disease such
CC as leukaemia, neurological disease such as multiple sclerosis and
CC bacterial or viral infections such as hepatitis. The present sequence is
CC the human 9E7LC light chain protein (variable region and J-region). This
CC sequence is used in the exemplification of the invention.
XX
SQ Sequence 130 AA;
Query Match 95.1%; Score 540; DB 8; Length 130;
Best Local Similarity 96.3%; Pred. No. 4.3e-36;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 80
Qy 61 RFGSGSGTDFTLTISLPEDEFAVYCCQRSNWPPTFTFGGTGVDIK 108
Db 81 RFGSGSGTDFTLTISLPEDEFAVYCCQRSNWPPTFTFGGTGVK 128

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Job time : 128.462 secs
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OM protein - protein search, using sw model  
Run on: December 28, 2005, 13:46:34 ; Search time 22.1538 Seconds  
(without alignments)  
469.057 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWNPPFTFGPTKVDIK 108

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528	93.0	114	2 S54905	Ig kappa chain V r
2	524.5	92.3	111	2 S23628	Ig kappa chain V r
3	519.5	91.5	144	2 PL0106	Ig kappa chain pre
4	517.5	91.1	128	2 A56701	Ig kappa chain V r
5	513.5	90.4	128	2 S40345	Ig kappa chain V-J
6	512.5	90.2	108	2 G44151	Ig kappa chain V r
7	510.5	89.9	129	2 S29627	Ig kappa chain V r
8	497.5	87.6	128	2 S40379	Ig kappa chain V-J
9	494.5	87.1	107	2 S57444	Ig kappa chain V-J
10	488.5	86.0	125	2 S40344	Ig kappa chain V-J
11	487	85.7	115	1 K3HUVG	Ig kappa chain pre
12	481	84.7	215	2 J50244	Ig kappa chain NIG
13	473.5	83.4	106	2 PC4282	Ig kappa chain (an
14	472.5	83.2	114	2 S46375	Ig kappa chain V-J
15	471	82.9	115	2 S11697	Ig kappa chain pre
16	470.5	82.8	117	2 S40362	Ig kappa chain - h
17	467.5	82.3	107	2 S34005	Ig kappa chain V r
18	467.5	82.3	129	2 S40363	Ig kappa chain - h
19	464	81.7	129	2 S40363	Ig kappa chain - h
20	462.5	81.4	128	2 S40343	Ig kappa chain V-J
21	462	81.3	130	2 S40360	Ig kappa chain - h
22	460	81.0	109	2 A30608	Ig kappa chain V-I
23	459	80.8	116	2 B26555	Ig kappa chain V-I
24	459	80.8	131	2 S40328	Ig kappa chain - h
25	459	80.8	215	2 J50242	Ig kappa chain NIG
26	458	80.6	109	2 H30601	Ig kappa chain V-I
27	458	80.6	109	2 B30601	Ig kappa chain V-I
28	458	80.6	109	2 PH0963	Ig kappa chain V r
29	456	80.3	92	2 S37506	Ig kappa chain V r

30	456	80.3	108	2 C30608	Ig kappa chain V-I
31	456	80.3	109	2 G30607	Ig kappa chain V-I
32	456	80.3	109	2 F30607	Ig kappa chain V-I
33	455.5	80.2	108	2 E30609	Ig kappa chain V-I
34	455	80.1	92	2 S37516	Ig kappa chain V r
35	455	80.1	109	2 C30601	Ig kappa chain V-I
36	455	80.1	109	2 D30601	Ig kappa chain V-I
37	454	79.9	128	2 S20636	Ig kappa chain V r
38	454	79.9	129	1 K3HUMA	Ig kappa chain pre
39	453	79.8	109	1 K3HUPM	Ig kappa chain V-I
40	453	79.8	110	2 S20635	Ig kappa chain V r
41	453	79.8	129	1 K3HUHI	Ig kappa chain pre
42	452	79.6	109	2 G30601	Ig kappa chain V-I
43	452	79.6	129	2 S46369	Ig light chain var
44	452	79.6	134	2 S38643	Ig kappa chain V r
45	448	78.9	108	2 B30608	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S54905  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S54905  
R:Esposito, G.; Traboni, C.  
submitted to the EMBL Data Library, November 1994  
A:Description: Cloning and sequencing of cDNA coding for the variable domains of a human  
A:Reference number: S54905  
A:Accession: S54905  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-114 <ESP>  
A:Cross-references: UNIPARC:UPI000011620A; EMBL:X82934; NID:G809554; PIDN:CAA58108.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 528; DB 2; Length 114;  
Best Local Similarity 92.6%; Pred. No. 5e-39;  
Matches 100; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLA	YQKPGQAPRLIYDASNRATGIPA 60
Db	1	DVMTQSPATLSLSPGERATLSCRASQSVSYLA	YQKPGQAPRLIYDASRRATGIPA 60
Qy	61	RFGSGSGTDTLTISLPEDEFAVYQCQRSNHPP	FTFGPTKVDIK 108
Db	61	RFGSGSGTDTLTISLPEDEFAVYQCQRSNHPP	LTFTGGTKVEIK 108

RESULT 2

S23628  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S23628  
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;  
J. Exp. Med. 175, 831-842, 1992  
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t  
A:Reference number: S23623; MUID:92156804; PMID:1740665  
A:Accession: S23628  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-111 <OLE>  
A:Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:G34022; PIDN:CAA42226.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 524.5; DB 2; Length 111;

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Best Local Similarity 95.4%; Pred. NO. 9.8e-39;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPPFTFGGKTKVDIK 108
Db 61 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNW-PWTFGGGKTKVEIK 107

RESULT 3
S40106
Ig kappa chain precursor V-J-C region (LSI) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: P40106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: P40106; MUID:89235583; PMID:2541221
A:Accession: P40106
A:Molecule type: mRNA
A:Residues: 1-144 <SIL>
A:Cross-references: UNIPARC:UPI00001767A2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 91.5%; Score 519.5; DB 2; Length 144;
Best Local Similarity 94.4%; Pred. No. 3.4e-38;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPPFTFGGKTKVDIK 108
Db 81 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNW-PLTFGGGKTKVEIK 127

RESULT 4
A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are ne
A:Reference number: A56701; MUID:95279371; PMID:7759488
A:Accession: A56701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: UNIPARC:UPI0000113B26; GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 517.5; DB 2; Length 128;
Best Local Similarity 94.4%; Pred. NO. 4.5e-38;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
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Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPPFTFGGKTKVDIK 108
Db 81 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPR-SFGGGKTKVEIK 127

RESULT 5
S40345
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40345
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40345
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: UNIPARC:UPI000011615F; EMBL:X72455; NID:g441378; PIDN:CAA51123.1; PI:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 90.4%; Score 513.5; DB 2; Length 128;
Best Local Similarity 91.7%; Pred. No. 1e-37;
Matches 100; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPA 60
Db 17 EIVLTQSPATLSLSPGERATLSCRASQSVRIYLAWYQKQPGQAPRLLIYDASNRATGIPA 76

Qy 61 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPP-FTFGGKTKVDIK 108
Db 77 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPPTLTFGGGKTKVEK 125

RESULT 6
G44151
Ig kappa chain V region (JM-10) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: G44151
R:Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pya
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746; PMID:1373487
A:Accession: G44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-108 <ZBB>
A:Cross-references: UNIPARC:UPI00001139AC; GB:M88317; NID:g183968; PIDN:AAA35975.1; PID:
A>Note: nucleotide translation not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 512.5; DB 2; Length 108;
Best Local Similarity 95.2%; Pred. No. 1e-37;
Matches 100; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 4 LTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPARFS 63
Db 3 LTQSPATLSLSPGERATLSCRASQSVSYLAWYQKQPGQAPRLLIYDASNRATGIPARFS 62

Qy 64 GSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPPFTFGGKTKVDIK 108
Db 63 GSGSGTDFTLTISISLEPEDFAVYYCQQRSNWPP-SFGGGKTKVEIK 106
```

## RESULT 7

S29627  
Ig kappa chain V region (60.3 hybridoma) - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34110; S29627  
R:Walls, M.A.; Hsiao, K.; Harris, L.J.  
Nucleic Acids Res. 21, 2921-2929, 1993  
A:Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains with human sequences  
A:Reference number: S34110; MUID:93324379; PMID:8332501  
A:Accession: S34110  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <WA2>  
A:Cross-references: UNIPARC:UPI000011649A; EMBL:Z17330; NID:938511; PID:CAA78978.1; PID:CAA78978.1; PID:CAA78978.1  
A:Note: human sequences cloned and sequenced prior to expression in mouse myeloma cells  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
C:Genetics:  
A:introns: 17/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 510.5; DB 2; Length 129;  
Best Local Similarity 92.7%; Pred. No. 1.8e-37;  
Matches 101; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 60  
|||  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 80  
|||  
Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSNWPPFTFGPGTKVDIK 108  
|||  
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSDNPPGATFGGKVEIK 129  
|||

## RESULT 8

S40379  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40379  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40379  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-128 <KLE>  
A:Cross-references: UNIPARC:UPI0000116181; EMBL:X72489; NID:9441446; PID:CAA51157.1; PID:CAA51157.1; PID:CAA51157.1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 497.5; DB 2; Length 128;  
Best Local Similarity 90.7%; Pred. No. 2.4e-36;  
Matches 98; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 60  
|||  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 80  
|||  
Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSNWPPFTFGPGTKVDIK 108  
|||  
Db 81 RFSGSGAGTDFTLTISLSEPEDFAVYVYCOQRSKW-PWTFGGGKVEIK 127  
|||

## RESULT 9

S57444  
Ig kappa chain V-J region - human (fragment)  
C:Species: Homo sapiens (man)

C>Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S57444  
R:Paterson, G.; Wilson, G.; Kennedy, P.G.B.; Willison, H.J.  
submitted to the EMBL Data Library, June 1995  
A:Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropathy patients  
A:Reference number: S57408  
A:Accession: S57444  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <PAT>  
A:Cross-references: UNIPARC:UPI00001137AE; EMBL:X87898; NID:9871275; PID:CAA61149.1; PID:CAA61149.1; PID:CAA61149.1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 494.5; DB 2; Length 107;  
Best Local Similarity 89.8%; Pred. No. 3.7e-36;  
Matches 97; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 60  
|||  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 60  
|||  
Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSNWPPFTFGPGTKVDIK 108  
|||  
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSNWPP-TFGGQTNVESK 107  
|||

## RESULT 10

S40344  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40344  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40344  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: UNIPARC:UPI000011615E; EMBL:X72454; NID:9441376; PID:CAA51122.1; PID:CAA51122.1; PID:CAA51122.1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 488.5; DB 2; Length 125;  
Best Local Similarity 90.6%; Pred. No. 1.4e-35;  
Matches 96; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 60  
|||  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA 80  
|||  
Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSNWPPFTFGPGTKVD 106  
|||  
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQRSYW-PLTFGGGKVE 125  
|||

## RESULT 11

K3HUVG  
Ig kappa chain precursor V-III region (Vg) - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C:Accession: A01900  
R:Pech, M.; Zachau, H.G.  
Nucleic Acids Res. 12, 9229-9236, 1984  
A:Title: Immunoglobulin genes of different subgroups are interdigitated within the V-K 1  
A:Reference number: A93549; MUID:85087932; PMID:6440122  
A:Accession: A01900  
A:Molecule type: DNA  
A:Residues: 1-115 <PEC>  
A:Cross-references: UNIPROT:P04433; UNIPARC:UPI0000116D05; GB:X01668; GB:K02768; NID:933

A>Note: the sequence was determined from the germline gene

C:Genetics:  
A:Gene: GDB:IGKV3  
A:Cross-references: GDB:136266  
A:Map position: 2p12-2p11  
A:Introns: 17/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes: immunoglobulin V region; immunoglobulin homology  
C:Superfamily: heterotetramer; immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <MAT>  
F:21-43/Region: framework 1  
F:36-110/Domain: immunoglobulin homology <IMM>  
F:44-54/Region: complementarity-determining 1  
F:55-69/Region: framework 2  
F:70-76/Region: complementarity-determining 2  
F:77-108/Region: framework 3  
F:109-115/Region: complementarity-determining 3  
F:43-108/Disulfide bonds: #status predicted

Query Match 85.7%; Score 487; DB 1; Length 115;  
Best Local Similarity 98.9%; Pred. No. 1.8e-35;  
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 EIVLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 95  
Db 81 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 115

# RESULT 12

Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: J050244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Tsuboi, M.; et al. 1998. Submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amyloidosis  
A:Reference number: J050243  
A:Accession: J050244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
A:Cross-references: UNIPARC:UPI0000176982  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.7%; Score 481; DB 2; Length 215;  
Best Local Similarity 85.2%; Pred. No. 1.1e-34;  
Matches 92; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60  
Db 1 EIVLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 108  
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 115

# RESULT 13

Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 21-Jan-2000  
C:Accession: PC4282; PC4284  
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.  
Biochem. Biophys. Res. Commun. 232, 101-106, 1997  
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltrative

A:Reference number: PC4279; MUID:97236289; PMID:9125110  
A:Accession: PC4282  
A:Molecule type: protein  
A:Residues: 1-106 <SUZ>  
A:Cross-references: UNIPARC:UPI0000176E92  
A:Note: E-42  
A:Accession: PC4284  
A:Molecule type: protein  
A:Residues: 1-106 <SU2>  
A:Cross-references: UNIPARC:UPI0000176E92  
A:Note: E-56  
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren's syndrome, immunoglobulin V region; immunoglobulin homology  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 473.5; DB 2; Length 106;  
Best Local Similarity 85.8%; Pred. No. 2.4e-34;  
Matches 91; Conservative 8; Mismatches 6; Indels 1; Gaps 1;  
Qy 3 VLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIPARF 62  
Db 1 VLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIPARF 60  
Qy 63 SGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 108  
Db 61 SGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 105

# RESULT 14

S46375  
Ig kappa chain V-J region (T33-5) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
C:Accession: S46375; S38648  
R:Bensimon, C.; Chastagner, P.; Zouali, M.  
EMBO J. 13, 2951-2962, 1994  
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement  
A:Reference number: S46369; MUID:94313975; PMID:8039491  
A:Accession: S46375  
A:Molecule type: mRNA  
A:Residues: 1-114 <BEN>  
A:Cross-references: UNIPARC:UPI00001165A8; EMBL:Z27176; NID:9415967; PIDN:CAA81700.1; PI:270955  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:20-95/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 472.5; DB 2; Length 114;  
Best Local Similarity 85.3%; Pred. No. 3.2e-34;  
Matches 93; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIP 59  
Db 5 EIVLTQSPATLSLSPGERATLSCRSQSVSYLAWYQKPGQAPRLIIYDASNRATGIP 64

Qy 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 108  
Db 65 DRFSGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP 113

# RESULT 15

S11697  
Ig kappa chain precursor V-III region - human  
C:Species: Homo sapiens (man)  
C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S11697  
R:Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.  
J. Mol. Biol. 183, 291-299, 1985  
A:Title: A large section of the gene locus encoding human immunoglobulin variable region  
A:Reference number: S11697; MUID:85264787; PMID:3927006  
A:Accession: S11697  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-115 <PEC>



A;Cross-references: UNIPARC:UPI0000115E41; EMBL:X17264; NID:g37898; PIDN:CAA35168.1; PID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 471; DB 2; Length 115;  
Best Local Similarity 96.8%; Pred. NO. 4.3e-34;  
Matches 91; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RPSGSGGTDFTLTISLPEPDAFVYCCQQRSNW 94  
Db 81 RPSGSGGTDFTLTISLPEPDAFVYCCQQRSNW 114

Search completed: December 28, 2005, 14:04:03  
Job time : 23.1538 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2005, 13:44:24 ; Search time 137.077 Seconds  
(without alignments)  
555.871 Million cell updates/sec

Title: US-09-920-137f-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPPTFGPGTKVDIK 108

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	85.7	115	1 KV3I_HUMAN	P04433 homo sapien
2	479.5	84.4	108	2 Q9UL83_HUMAN	Q9UL83 homo sapien
3	474	83.5	129	1 KV3H_HUMAN	P04207 homo sapien
4	468	82.4	109	2 Q9UL85_HUMAN	Q9UL85 homo sapien
5	454	79.9	129	1 KV3L_HUMAN	P18135 homo sapien
6	453	79.8	109	1 KV3F_HUMAN	P01624 homo sapien
7	453	79.8	129	1 KV3M_HUMAN	P18136 homo sapien
8	449	79.0	109	2 Q9UL78_HUMAN	Q9UL78 homo sapien
9	448	78.9	109	1 KV3B_HUMAN	P01620 homo sapien
10	448	78.9	109	1 KV3D_HUMAN	Q9UL86 homo sapien
11	448	78.9	109	2 Q9UL86_HUMAN	Q9UL86 homo sapien
12	447.5	78.8	236	2 Q9PI18_HUMAN	Q9PI18 homo sapien
13	447	78.7	235	2 Q9P5F7_HUMAN	Q9P5F2 homo sapien
14	443.5	78.1	236	2 Q9P5S8_HUMAN	Q9P5S8 homo sapien
15	442	77.8	109	1 KV3E_HUMAN	P01623 homo sapien
16	442	77.8	235	2 Q6GMW0_HUMAN	Q6GMW0 homo sapien
17	431.5	76.0	128	1 KV3K_HUMAN	P06311 homo sapien
18	429	75.5	108	1 KV3A_HUMAN	P01619 homo sapien
19	428	75.4	109	1 KV3G_HUMAN	P04206 homo sapien
20	428	75.4	235	2 Q6GMV9_HUMAN	Q6GMV9 homo sapien
21	414.5	73.0	116	1 KV3J_HUMAN	P04434 homo sapien
22	411.5	72.4	100	1 KV3C_HUMAN	P01621 homo sapien
23	411.5	72.4	236	2 Q6GMX8_HUMAN	Q6GMX8 homo sapien
24	407.5	71.7	108	1 KV1M_HUMAN	P01605 homo sapien
25	401.5	70.7	244	2 Q65ZC8_HUMAN	Q65ZC8 homo sapien
26	398	70.1	107	1 KV1D_HUMAN	P01596 homo sapien
27	397.5	70.0	108	1 KV1V_HUMAN	P04430 homo sapien
28	397.5	70.0	240	2 Q65ZC9_HUMAN	Q65ZC9 homo sapien
29	396.5	69.8	236	2 Q9PIH7_HUMAN	Q9PIH7 homo sapien
30	393.5	69.3	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien
31	392	69.0	107	2 Q96SA9_HUMAN	Q96SA9 homo sapien

32	390.5	68.8	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
33	385.5	67.9	108	1 KV1H_HUMAN	P01600 homo sapien
34	385.5	67.9	234	2 Q569I9_HUMAN	Q569I9 homo sapien
35	385	67.8	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
36	384.5	67.7	111	1 KV3M_MOUSE	P01665 mus musculus
37	383.5	67.5	134	1 KV4C_HUMAN	P06314 homo sapien
38	382.5	67.3	108	1 KV1K_HUMAN	P01603 homo sapien
39	381.5	67.2	108	1 KV1L_HUMAN	P01604 homo sapien
40	380.5	67.0	111	1 KV3O_MOUSE	P01667 mus musculus
41	380.5	67.0	236	2 Q6GMW1_HUMAN	Q6GMW1 homo sapien
42	379.5	66.8	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
43	378.5	66.6	111	1 KV3L_MOUSE	P01664 mus musculus
44	377.5	66.5	108	1 KV1E_HUMAN	P01597 homo sapien
45	377.5	66.5	111	1 KV3H_MOUSE	P01660 mus musculus

ALIGNMENTS

RESULT 1

ID	KV3I_HUMAN	STANDARD;	PRT;	115 AA.
AC	P04433;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig kappa chain V-III region Vg precursor (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=85087932; PubMed=6440122;			
RA	Pech M., Zachau H.G.;			
RT	"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.";			
RL	Nucleic Acids Res. 12:9229-9236(1984).			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	-----			
DR	EMBL; X01668; ; NOT_ANNOTATED_CDS; Genomic_DNA.			
DR	PIR; A01900; K3HUVG.			
DR	HSSP; P01625; 185Q.			
DR	SMR; P04433; 21-115.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; P:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 >115			
FT	REGION 21 43			
FT	REGION 44 54			
FT	REGION 55 69			
FT	REGION 70 76			
FT	REGION 77 108			
FT	REGION 109 115			
FT	DISULFID 43 108			
FT	NON_TER 115 115			
SQ	SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;			

Query Match 85.7%; Score 487; DB 1; Length 115;  
Best Local Similarity 98.9%; Pred No. 9,5e-43;  
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
|||
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRTATGIPA 80
|||

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 95
|||
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 115
|||

RESULT 2
Q9UL83 HUMAN
ID Q9UL83 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.N.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035031; AAD56267.1; -; mRNA.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P01625; 1LVE.
DR SMR; P04207; 21-129.
DR InterPro; IPR007110; IG-Like.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 84.4%; Score 479.5; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
|||
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYCHSTRATGIPA 60
|||

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPTFGTGKVDIK 108
|||
Db 61 RFSGSGSGTEFTLTISLQFEDFAVYQCQHYNNW-PPTFGTGKVDIK 107
|||

RESULT 3
KV3H HUMAN
ID KV3H HUMAN STANDARD; PRT; 129 AA.
AC P04207;
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DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik P.R., Sorge J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,
RA Clodfien R., Carson D.A.;
RA "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M12740; AAA58992.1; -; Genomic_DNA.
CC HSSP; P01625; 1LVE.
CC SMR; P04207; 21-129.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-Like.
CC SMART; SM00406; IGV; 1_v.
CC PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT REGION 21 129 Ig kappa chain V-III region CLL.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Complementarity-determining-2.
FT REGION 109 118 Framework-3.
FT REGION 119 129 Complementarity-determining-3.
FT DISULFID 43 108 By similarity.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 83.5%; Score 474; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 2.5e-41;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
|||
Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 80
|||

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPTFGTGKVDIK 108
|||
Db 81 RFSGSGSGTEFTLTISLQFEDFAVYQCQHYNNW-PPTFGTGKVDIK 128
|||

RESULT 4
Q9UL85 HUMAN
ID Q9UL85 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```

OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035029; AAD56265.1; -; mRNA.  
 DR PIR; D30609; D30609.  
 DR HSSP; P01625; 1EK3.  
 DR SMR; Q9UL85; 1-109.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 109  
 FT NON\_TER 109  
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43B7C7AFACCC CRC64;  
 Query Match 82.4%; Score 468; DB 2; Length 109;  
 Best Local Similarity 82.4%; Pred. No. 8.5e-41;  
 Matches 89; Conservative 10; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVYSLAWYQKPKQAPRLLIYDASNRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCWASQISNLAWYQKPKQAPRLLIYGASTRATGIPA 60  
 QY 61 RPSGSGCTDFTLTISLPEDEFAVYCYQQRSNWPPFTFGCTKVDIK 108  
 DB 61 RPSGSGCTEFTLTISLQSDFAIYHCQYNSWPPFTFGGTVKEIK 108  
 RESULT 5  
 KV3L\_HUMAN  
 ID KV3L\_HUMAN STANDARD; PRT; 129 AA.  
 AC P18135;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-III region HAH precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";  
 RL J. Exp. Med. 167:840-852(1988).  
 CC -1- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC PIR; P10022; K3HUHA.  
 DR HSSP; P01625; 1EEQ.  
 DR SMR; P18135; 21-129.  
 DR Ensembl; ENSG00000169769; Homo sapiens.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM003596; IG\_v.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129  
 FT REGION 21 43  
 FT REGION 44 55  
 FT REGION 56 70  
 FT REGION 71 77  
 FT REGION 78 109  
 FT REGION 110 118  
 FT REGION 119 129  
 FT DISULFID 43 109  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C529272774D0 CRC64;  
 Query Match 79.9%; Score 454; DB 1; Length 129;  
 Best Local Similarity 86.2%; Pred. No. 3e-39;  
 Matches 94; Conservative 2; Mismatches 11; Indels 2; Gaps 2;  
 QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVYSLAWYQKPKQAPRLLIYDASNRATGIP 59  
 DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPKQAPRLLIYGASSRATGIP 80  
 QY 60 ARFGSGSGTDTLTISLPEDEFAVYCYQQRSNWPPFTFGCTKVDIK 108  
 DB 81 DRFGSGSGTDTLTISLPEDEFAVYCYQYGT-SPRTFGGTVKEIK 128  
 RESULT 6  
 KV3F\_HUMAN  
 ID KV3F\_HUMAN STANDARD; PRT; 109 AA.  
 AC P01624;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-III region POM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=76276460; PubMed=60899;  
 RA Klapper D.G., Capra J.D.;  
 RT "The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";  
 RL Ann. Immunol. (Paris) 127C:261-271(1976).  
 CC -1- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC PIR; A01897; K3HUPM.  
 DR HSSP; P01625; 1LVE.  
 DR SMR; P01624; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89  
 By similarity.

FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11922 MW; 62821DDCGA8ABA86 CRC64;

Query Match 79.8%; Score 453; DB 1; Length 109;  
Best Local Similarity 81.7%; Pred. No. 3.le-39;  
Matches 89; Conservative 9; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQKPGQAPRLLIYDASNRATGIP 59  
Db 1 EIVMTQSPVTLSPGERATLSCRASQSVINSYLAAYQKPGSPRLLIYGASTRAATGIP 60

Qy 60 ARFGSGSGTDFTLTISLSEPEDFAVYCCQQRSNWPPFTFGGKTKVDIK 108  
Db 61 ARFGSGSGTDFTLTISLSEPEDFAVYCCQQRNWP-TFGGTRVEIK 108

RESULT 7  
KV3M HUMAN  
ID KV3M HUMAN STANDARD; PRT; 129 AA.  
AC P18136;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-III region HIC precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";  
RL J. Exp. Med. 167:840-852(1988).  
CC -I- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
CC  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC  
CC PIR; P10021; K3HUHI.  
DR HSSP; P01625; 1ERQ.  
DR SMR; P18136; 21-129.  
DR Ensembl; ENSG00000169769; Homo sapiens.  
DR GO; GO:000576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 Ig kappa chain V-III region HIC.  
FT REGION 21 43 Framework-1.  
FT REGION 44 55 Complementarity-determining-1.  
FT REGION 56 70 Framework-2.  
FT REGION 71 77 Complementarity-determining-2.  
FT REGION 78 109 Framework-3.  
FT REGION 110 118 Complementarity-determining-3.  
FT REGION 119 129 JKL segment.  
FT DISULFID 43 109 By similarity.  
FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;

Query Match 79.8%; Score 453; DB 1; Length 129;

Best Local Similarity 85.3%; Pred. No. 3.8e-39;  
Matches 93; Conservative 4; Mismatches 10; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQKPGQAPRLLIYDASNRATGIP 59  
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLLIYGASTRATGIP 80

Qy 60 ARFGSGSGTDFTLTISLSEPEDFAVYCCQQRSNWPPFTFGGKTKVDIK 108  
Db 81 DRFGSGSGTDFTLTISLSEPEDFAVYCCQYGS-SPTTFGGTKVEIK 128

RESULT 8  
Q9UL78 HUMAN  
ID Q9UL78 HUMAN PRELIMINARY; PRT; 109 AA.  
AC Q9UL78;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1373487;  
RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R., Dedraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;  
RT "Human combinatorial antibody libraries to hepatitis B surface antigen.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8436174;  
RA Wagner S.D., Luzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation.";  
RL Eur. J. Immunol. 23:391-397(1993).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1552291;  
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;  
RT "Evidence for somatic selection of natural autoantibodies.";  
RL J. Exp. Med. 175:983-991(1992).  
DR EMBL; AF035036; AAD56272.1; -, mRNA.  
DR PIR; A30601; A30601.  
DR PIR; A30608; A30608.  
DR PIR; B30601; B30601.  
DR PIR; B30607; B30607.  
DR PIR; C30601; C30601.  
DR PIR; C30607; C30607.  
DR PIR; C30608; C30608.  
DR PIR; D30601; D30601.  
DR PIR; D30607; D30607.  
DR PIR; D30608; D30608.  
DR PIR; F30607; F30607.  
DR PIR; F30608; F30608.  
DR PIR; G30601; G30601.  
DR PIR; G30608; G30608.  
DR PIR; H30607; H30607.  
DR PIR; H30608; H30608.

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DR PIR: H44151; H44151.
DR PIR: I30601; I30601.
DR PIR: PH0963; PH0963.
DR PIR: PH0964; PH0964.
DR PIR: PH0965; PH0965.
DR PIR: S33988; S33988.
DR PIR: S34096; S34096.
DR HSSP: P01625; 1EX3.
DR SMR: Q9UL78; 1-109.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 79.0%; Score 449; DB 2; Length 109;
Best Local Similarity 85.3%; Pred. No. 8.1e-39;
Matches 93; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYDASNRATGIP 60

Qy 60 ARFSGSGGTDFTLTISLLEPEDFAVYCCQQRSNWPPFTFGGTVKDIK 108
Db 61 DRFSGSGGTDFTLTISRLEPDCAVYCCQYGS-SPLTFGGGTVKEIK 108

RESULT 9
KV3B HUMAN
ID KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region SIg.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN PROTEIN SEQUENCE.
RP MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR: A01892; K3HUSI.
CC HSSP: P01620; 1-109.
CC SMR: P01620; 1-109.
CC GO: GO:0005576; C:extracellular region; NAS.
CC GO: GO:0003823; F:antigen binding; NAS.
CC GO: GO:0006955; P:immune response; NAS.
CC InterPro: IPR007110; Ig-like.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin V region.
CC DISULFID 23 89 By similarity.
CC
CC PIR: A01892; K3HUSI.
CC HSSP: P01625; 1LVE.
CC SMR: P01620; 1-109.
CC GO: GO:0005576; C:extracellular region; NAS.
CC GO: GO:0003823; F:antigen binding; NAS.
CC GO: GO:0006955; P:immune response; NAS.
CC InterPro: IPR007110; Ig-like.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin V region.
CC DISULFID 23 89 By similarity.

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FT NON_TER 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 78.9%; Score 448; DB 1; Length 109;
Best Local Similarity 84.4%; Pred. No. 1e-38;
Matches 92; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYDASNRATGIP 60

Qy 60 ARFSGSGGTDFTLTISLLEPEDFAVYCCQQRSNWPPFTFGGTVKDIK 108
Db 61 DRFSGSGGTDFTLTISRLEPDFAVYCCQYGS-SPOTFGGSKVEIK 108

RESULT 10
KV3D HUMAN
ID KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN PROTEIN SEQUENCE.
RP MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT TI). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR: A01895; K3HUTI.
CC HSSP: P01625; 1LVE.
CC SMR: P01622; 1-109.
CC GO: GO:0005576; C:extracellular region; NAS.
CC GO: GO:0003823; F:antigen binding; NAS.
CC GO: GO:0006955; P:immune response; NAS.
CC InterPro: IPR007110; Ig-like.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin V region.
CC DISULFID 23 89 By similarity.
CC
CC NON_TER 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 78.9%; Score 448; DB 1; Length 109;
Best Local Similarity 84.4%; Pred. No. 1e-38;
Matches 92; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYDASNRATGIP 60

Qy 60 ARFSGSGGTDFTLTISLLEPEDFAVYCCQQRSNWPPFTFGGTVKDIK 108
Db 61 DRFSGSGGTDFTLTISRLEPDFAVYCCQYGS-SPOTFGGSKVEIK 108

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61 DRFGSGSGTDTLTISRLEPEDFAVYYCQYGS-SPSTFGQTKVDIK 108

## RESULT 11

Q6PJF2\_HUMAN  
ID Q6PJF2\_HUMAN PRELIMINARY; PRT; 109 AA.  
AC Q6PJF2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin kappa chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035028; AAD56264.1; -; mRNA.  
DR PIR; B30607; B30607.  
DR PIR; I30601; I30601.  
DR HSSP; P01625; 1EK3.  
DR SMR; P01625; 1EK3.  
DR SMR; Q9UL86; 1-109.  
DR InterPro; ENSG00000169769; Homo sapiens.  
DR EMBL; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 109  
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 78.9%; Score 448; DB 2; Length 109;  
Best Local Similarity 85.3%; Pred. No. 1e-38;  
Matches 93; Conservative 2; Mismatches 12; Indels 2; Gaps 2;  
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-VSYLAWYQKQPGQAPRLIYDASNRATGIP 59  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKQPGQAPRLIYDASNRATGIP 60  
Qy 60 ARFGSGSGTDTLTISRLEPEDFAVYYCQYGS-SPSTFGQTKVDIK 108  
Db 61 DRFGSGSGTDTLTISRLEPEDFAVYYCQYGS-SITFGGKVDIK 108

## RESULT 12

Q6PJF2\_HUMAN  
ID Q6PJF2\_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6PJF2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC032451; AAH32451.1; -; mRNA.  
DR HSSP; P01837; 1KCU.  
DR SMR; Q6PIL8; 21-236.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00407; IGc1; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;  
Query Match 78.8%; Score 447.5; DB 2; Length 236;  
Best Local Similarity 82.6%; Pred. No. 2.9e-38;  
Matches 90; Conservative 4; Mismatches 14; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-VSYLAWYQKQPGQAPRLIYDASNRATGIP 59  
Db 21 ENVLTQSPGTLSPGERATLSCRASQSLSSYLAWYQKQPGQAPRLIYGVSSRATGIP 80  
Qy 60 ARFGSGSGTDTLTISRLEPEDFAVYYCQYGS-SPSTFGQTKVDIK 108  
Db 81 DRFGSGSGTDTLTISRLEPEDFAVYYCQYGS-SITFGGKVDIK 129  
RESULT 13  
Q6PJF2\_HUMAN  
ID Q6PJF2\_HUMAN PRELIMINARY; PRT; 235 AA.  
AC Q6PJF2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA



RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RA Strauberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016380; AAH16380.1; -; mRNA.  
DR HSSP; P01837; IKCU.  
DR SMR; O6PJF2; 21-235.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;  
Query Match 78.7%; Score 447; DB 2; Length 235;  
Best Local Similarity 84.4%; Pred. No. 3.3e-38;  
Matches 92; Conservative 5; Mismatches 10; Indels 2; Gaps 2;  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVY- YLAWYQKPGQAPRLIYDASNRATGIP 59  
DB 21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQKPGAPRLIMFGSSSRATGIP 80  
QY 60 ARFSGSGSGTFTLTITSLPEDEPAVYCCQQRNWPPTFGPGTKVDIK 108  
DB 81 DRFSGSGSGTFTLTITSLPEDEPAVYCCQYGS- SQCTFGPGTKVDIK 128  
RESULT 14  
KV3E HUMAN  
ID Q6P5S8 HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6P5S8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Glandular pool- thyroid;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Glandular pool- thyroid;  
RA Strauberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC062704; AAH62704.1; -; mRNA.  
DR HSSP; P01837; IKCU.  
DR SMR; O6P5S8; 21-236.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;  
Query Match 78.1%; Score 443.5; DB 2; Length 236;  
Best Local Similarity 79.8%; Pred. No. 7.6e-36;  
Matches 87; Conservative 9; Mismatches 12; Indels 1; Gaps 1;  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVY- SYLAWYQKPGQAPRLIYDASNRATGIP 59  
DB 21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQKPGAPRLIYDASNRATGIP 80  
QY 60 ARFSGSGSGTFTLTITSLPEDEPAVYCCQQRNWPPTFGPGTKVDIK 108  
DB 81 DRFSGSGSGTFTLTITSLPEDEPAVYCCQYGS- SQCTFGPGTRVEIK 129  
RESULT 15  
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ID KV3E HUMAN STANDARD; PRT; 109 AA.  
AC P01623;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-III region WOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=82046598; PubMed=6794615;  
RA Andrews D.W., Capra J.D.;  
RT "Amino acid sequence of the variable regions of light chains from two  
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
RT group";  
RL Biochemistry 20:5816-5822 (1981).  
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma  
CC globulin activity.  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
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DR PIR; A01896; K3HJWL.  
 DR HSSP; P01625; 1LVE.  
 DR SMR; P01623; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89 By similarity.  
 FT NON\_TER 109 109  
 SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEEE CRC64;

Query Match 77.8%; Score 442; DB 1; Length 109;  
 Best Local Similarity 84.4%; Pred. No. 4.3e-38;  
 Matches 92; Conservative 3; Mismatches 12; Indels 2; Gaps 2;  
 Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVYS-YLAWYQOKFGQAPRLIIYDASNRATGIP 59  
 Db 1 EIVLTQSPGTLTLSPGERATLSCRASQSVSSGVLGWYQOKFGQAPRLIIYGASSRATGIP 60  
 Qy 60 ARFSGSGSGTDFTLTITISLSEPEDFAVYCCQQRSNWPPFTFGPGTKVDIK 108  
 Db 61 DRFSGSGSGTDFTLTITISLSEPEDFAVYCCQYQYGLGR-TFGQGTKEIK 108

Search completed: December 28, 2005, 14:03:09  
 Job time : 138.077 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:53:15 ; Search time 30 Seconds  
(without alignments)  
297.632 Million cell updates/sec

Title: US-09-920-137f-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPPTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgm2\_6/ptodata/1/iaa/6-COMB.pep.\*  
3: /cgm2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PCTUS-COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	92.2	224	2	US-09-456-090A-46
2	523.5	92.2	224	2	US-09-453-234-46
3	522.5	92.0	107	2	US-09-434-870-2
4	518.5	91.3	224	2	US-09-456-090A-82
5	518.5	91.3	224	2	US-09-456-090A-88
6	518.5	91.3	224	2	US-09-456-090A-90
7	518.5	91.3	224	2	US-09-453-234-82
8	518.5	91.3	224	2	US-09-453-234-88
9	518.5	91.3	224	2	US-09-453-234-90
10	517.5	91.1	224	2	US-09-456-090A-36
11	517.5	91.1	224	2	US-09-453-234-36
12	514.5	90.6	224	2	US-09-456-090A-84
13	514.5	90.6	224	2	US-09-453-234-84
14	509.5	89.7	107	2	US-09-438-954-40
15	493.5	86.9	226	2	US-09-456-090A-38
16	493.5	86.9	226	2	US-09-453-234-38
17	491.5	86.5	234	2	US-09-848-832-4
18	489	86.1	105	2	US-08-635-109-6
19	489	86.1	105	2	US-08-844-215-9
20	489	86.1	117	2	US-09-203-768A-4
21	487	85.7	95	2	US-10-194-975-86
22	487	85.7	115	1	US-08-053-131-179
23	487	85.7	115	1	US-08-096-762-179
24	487	85.7	115	2	US-09-042-353-42
25	487	85.7	115	2	US-08-758-417A-307
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28 479.5 84.4 226 2 US-09-456-090A-42 Sequence 42, Appl
29 479.5 84.4 226 2 US-09-453-234-42 Sequence 42, Appl
30 474 83.5 110 2 US-09-025-769B-30 Sequence 30, Appl
31 474 83.5 110 2 US-09-025-769B-47 Sequence 47, Appl
32 474 83.5 110 2 US-09-490-070A-30 Sequence 30, Appl
33 474 83.5 110 2 US-09-490-070A-47 Sequence 47, Appl
34 474 83.5 110 2 US-09-490-153-30 Sequence 30, Appl
35 474 83.5 110 2 US-09-490-153-47 Sequence 47, Appl
36 474 83.5 110 2 US-09-490-324-30 Sequence 30, Appl
37 474 83.5 110 2 US-09-490-324-47 Sequence 47, Appl
38 473.5 83.4 226 2 US-09-456-090A-50 Sequence 50, Appl
39 473.5 83.4 226 2 US-09-456-090A-86 Sequence 86, Appl
40 473.5 83.4 226 2 US-09-453-234-50 Sequence 50, Appl
41 473.5 83.4 226 2 US-09-453-234-86 Sequence 86, Appl
42 472.5 83.2 226 2 US-09-456-090A-74 Sequence 74, Appl
43 472.5 83.2 226 2 US-09-453-234-74 Sequence 74, Appl
44 471.5 83.0 234 2 US-09-472-087-17 Sequence 17, Appl
45 471.5 83.0 234 2 US-09-472-087-69 Sequence 69, Appl

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## ALIGNMENTS

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RESULT 1
US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkira, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MI-10L
US-09-456-090A-46

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Query Match 92.2%; Score 523.5; DB 2; Length 224;
Best Local Similarity 93.5%; Pred. No. 2e-42;
Matches 101; Conservative 4; Mismatches 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
Db 1 DVNVTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGSGTDFTLTISLPEDEFAVYYCQQRNWPPTFGPGTKVDIK 108
Db 61 RFSGSGSGTDFTLTISLPEDEFAVYYCQQRNWPPTFGPGTKVVEIK 107

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RESULT 2
US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkira, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453.234
; CURRENT FILING DATE: 1999-12-01

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; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match          92.2%; Score 523.5; DB 2; Length 224;
Best Local Similarity 93.5%; Pred. No. 2e-42;
Matches 101; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
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Db 1 DVNMTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRSNWPPFTFGGTKVVEIK 107

RESULT 3
US-09-434-870-2
; Sequence 2, Application US/09434870
; Patent No. 6849425
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffery
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-06352
; CURRENT APPLICATION NUMBER: US/09/434,870
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/159,689
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-434-870-2

Query Match          92.0%; Score 522.5; DB 2; Length 107;
Best Local Similarity 95.4%; Pred. No. 1.1e-42;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRSNW-PLTFGGGTKVVEIK 107

RESULT 4
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRNWP-TFGGGTKVVEIK 107

RESULT 5
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 RFGSGSGTDTFTLTISLPEDFAVYYCQQRNWP-TFGGGTKVVEIK 107

RESULT 6
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFGSGSGTDFLTITISLPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 108
Db 61 RFGSGSGTDFLTITISLPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 107

RESULT 7
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFGSGSGTDFLTITISLPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 108
Db 61 RFGSGSGTDFLTITISLPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 107

RESULT 8
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; FILE REFERENCE: 020015-000200US

; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFGSGSGTDFLTITISLPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 108
Db 61 RFGSGSGTDFLTITISLPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 107

RESULT 10
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Human Antibodies AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
```



; APPLICANT: YOON, Sung Kwan  
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME  
; FILE REFERENCE: 1303-124P  
; CURRENT APPLICATION NUMBER: US/09/438,954  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Variable  
; OTHER INFORMATION: region of light chain of human antibody (X82934)  
US-09-438-954-40

Query Match 89.7%; Score 509.5; DB 2; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1.9e-41;  
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLIIYDASNRATGIPA 60  
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 DVVMTQSPATLSVSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLIIYDASNRATGIPA 60  
QY 61 RPSGSGSGTDFTLTISLSEDPEDFAVYQCQRSNWPPPTFGPGTKVDIK 108  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 RPSGSGSGTDFTLTISLSEDPEDFAVYQCQRSNWPPPTFGPGTKVKEIK 107

## RESULT 15

US-09-456-090A-38  
; Sequence 38, Application US/09456090A  
; Patent No. 6680209  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-000200US  
; CURRENT APPLICATION NUMBER: US/09/456,090A  
; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-3L  
US-09-456-090A-38

Query Match 86.9%; Score 493.5; DB 2; Length 226;  
Best Local Similarity 89.9%; Pred. No. 1.5e-39;  
Matches 98; Conservative 3; Mismatches 7; Indels 1; Gaps 1;  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQQKPGQAPRLIIYDASNRATGIP 59  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIP 60  
QY 60 RPSGSGSGTDFTLTISLSEDPEDFAVYQCQRSNWPPPTFGPGTKVDIK 108  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 DRPSGSGSGTDFTLTISRLEPEDFAVYCCQYQSSPPPTFGPGTKVDIK 109

Search completed: December 28, 2005, 14:05:14  
Job time : 30 secs

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OM protein - protein search, using sw model

Run on: December 28, 2005, 14:03:21 ; Search time 102.462 Seconds  
(without alignments)  
440.415 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPPTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	98.4	108	3	US-09-920-267C-8
2	559	98.4	108	4	US-10-305-347A-8
3	559	98.4	108	4	US-10-720-323-8
4	559	98.4	108	5	US-10-954-900A-8
5	541	95.2	108	6	US-11-009-731-90
6	541	95.2	109	4	US-10-408-901-24
7	541	95.2	215	4	US-10-408-901-48
8	540	95.1	128	4	US-10-656-769-12
9	540	95.1	130	4	US-10-394-471B-16
10	540	95.1	235	4	US-10-656-769-38
11	539	94.9	109	4	US-10-408-901-8
12	539	94.9	215	4	US-10-408-901-32
13	538	94.7	108	4	US-10-173-551-9
14	536	94.4	108	5	US-10-886-838-4
15	535	94.2	108	6	US-11-021-715-101
16	534	94.0	108	6	US-11-009-731-85
17	534	94.0	108	6	US-11-102-403-9
18	534	94.0	108	6	US-11-102-403-11
19	534	94.0	109	4	US-10-408-901-16
20	534	94.0	109	4	US-10-408-901-28
21	534	94.0	215	4	US-10-408-901-40
22	534	94.0	215	4	US-10-408-901-52
23	531.5	93.6	129	4	US-10-478-056-19
24	529.5	93.2	107	4	US-10-251-085B-142
25	529.5	93.2	107	4	US-10-737-252-142
26	529.5	93.2	236	5	US-10-961-567A-6
27	529	93.1	251	3	US-09-880-748-1049

28	529	93.1	251	4	US-10-293-418-1049	Sequence 1049, Ap
29	524.5	92.3	107	5	US-10-891-658-91	Sequence 91, Appl
30	524	92.3	108	5	US-10-886-838-2	Sequence 2, Appl
31	524	92.3	108	6	US-11-009-731-92	Sequence 92, Appl
32	523.5	92.2	107	3	US-09-791-153A-69	Sequence 69, Appl
33	523.5	92.2	224	3	US-09-453-234-46	Sequence 46, Appl
34	523	92.1	108	4	US-10-173-551-19	Sequence 19, Appl
35	523	92.1	130	4	US-10-443-466A-25	Sequence 25, Appl
36	522.5	92.0	107	3	US-09-791-153A-71	Sequence 71, Appl
37	522.5	92.0	107	3	US-09-982-464-2	Sequence 2, Appl
38	522.5	92.0	107	5	US-10-697-399-2	Sequence 2, Appl
39	522.5	92.0	107	5	US-10-697-400-2	Sequence 2, Appl
40	522.5	92.0	107	5	US-10-911-838-14	Sequence 14, Appl
41	522.5	92.0	107	5	US-10-911-838-21	Sequence 21, Appl
42	522.5	92.0	107	6	US-11-102-403-3	Sequence 3, Appl
43	522.5	92.0	128	4	US-10-478-056-31	Sequence 55, Appl
44	522.5	92.0	139	4	US-10-687-799-55	Sequence 55, Appl
45	522	91.9	106	6	US-11-021-715-99	Sequence 99, Appl

## ALIGNMENTS

RESULT 1  
US-09-920-267C-8  
; Sequence 8, Application US/09920267C  
; Publication No. US20030040044A1  
; GENERAL INFORMATION:  
; APPLICANT: Centocor, Inc.  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Trikha, Mohit  
; APPLICANT: Snyder, Linda  
; APPLICANT: Nakada, Marian  
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES  
; FILE REFERENCE: CEN 249  
; CURRENT APPLICATION NUMBER: US/09/920,267C  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/223,363  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-267C-8

Query Match	98.4%;	Score 559;	DB 3;	Length 108;
Best Local Similarity	99.1%;	Pred. NO. 1.8e-41;		
Matches 107;	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;
QY	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLIYDASNRATGIPA	60	
Db	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLIYDASNRATGIPA	60	
QY	61	RFSGGSGTDTLTITISLPEPEFAVYCCQQRNWPPTFGPGTKVDIK	108	
Db	61	RFSGGSGTDTLTITISLPEPEFAVYCCQQRNWPPTFGPGTKVDIK	108	

RESULT 2  
US-10-305-347A-8  
; Sequence 8, Application US/10305347A  
; Publication No. US20030143603A1  
; GENERAL INFORMATION:  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Bernie Scallan  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN5005  
; CURRENT APPLICATION NUMBER: US/10/305,347A  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver 3.0

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; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-8

Query Match          98.4%; Score 559; DB 4; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.8e-41;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||

Qy 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||

RESULT 3
US-10-720-323-8
; Sequence 8, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-8

Query Match          98.4%; Score 559; DB 4; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.8e-41;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||

Qy 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||

RESULT 4
US-10-954-900A-8
; Sequence 8, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallan
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
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; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-8

Query Match          98.4%; Score 559; DB 5; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.8e-41;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||

Qy 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||

RESULT 5
US-11-009-731-90
; Sequence 90, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MX1-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-90

Query Match          95.2%; Score 541; DB 6; Length 108;
Best Local Similarity 95.4%; Pred. No. 6.7e-40;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||

Qy 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDTFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKLEIK 108
   |||||

RESULT 6
US-10-408-901-24
; Sequence 24, Application US/10408901
; Publication No. US2004002331A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
```

```
; APPLICANT: Elliott, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-24

Query Match          95.2%; Score 541; DB 4; Length 109;
Best Local Similarity 95.4%; Pred. No. 6.7e-40;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 7
US-10-408-901-48
; Sequence 48, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliott, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-48

Query Match          95.2%; Score 541; DB 4; Length 215;
Best Local Similarity 95.4%; Pred. No. 1.3e-39;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 8
US-10-656-769-12
; Sequence 12, Application US/10656769
; Publication No. US2004009712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
```

```
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-12

Query Match          95.1%; Score 540; DB 4; Length 128;
Best Local Similarity 96.3%; Pred. No. 9.6e-40;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 80

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 128

RESULT 9
US-10-394-471B-16
; Sequence 16, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallon, Bernard J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 16
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-16

Query Match          95.1%; Score 540; DB 4; Length 130;
Best Local Similarity 96.3%; Pred. No. 9.8e-40;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRTATGIPA 80

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 128

RESULT 10
US-10-656-769-38
; Sequence 38, Application US/10656769
; Publication No. US2004009712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
```

```
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-38

Query Match          95.1%; Score 540; DB 4; Length 235;
Best Local Similarity 96.3%; Pred. No. 1.7e-39;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGPTKVDIK 108
Db 81 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGGTVKEIK 128

RESULT 11
US-10-408-901-8
; Sequence 8, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Eliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-8

Query Match          94.9%; Score 539; DB 4; Length 109;
Best Local Similarity 94.4%; Pred. No. 1e-39;
Matches 102; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGPTKVDIK 108
Db 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGGTVKEIK 108

RESULT 12
US-10-408-901-32
; Sequence 32, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Eliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
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; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-32

Query Match          94.9%; Score 539; DB 4; Length 215;
Best Local Similarity 94.4%; Pred. No. 2e-39;
Matches 102; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGPTKVDIK 108
Db 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGGTVKEIK 108

RESULT 13
US-10-173-551-9
; Sequence 9, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855-2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDR1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)...(56)
; OTHER INFORMATION: CDR2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)...(98)
; OTHER INFORMATION: CDR3
US-10-173-551-9

Query Match          94.7%; Score 538; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 1.2e-39;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGPTKVDIK 108
Db 61 RFSGSGGTDFLTITISLPEDEFAVYYCQQRSNWPPFTFGGTVKEIK 108

RESULT 14
US-10-886-838-4
; Sequence 4, Application US/10886838
; Publication No. US20050008642A1
; GENERAL INFORMATION:
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; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,838
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-838-4
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Query Match          94.4%; Score 536; DB 5; Length 108;
Best Local Similarity 95.4%; Pred. No. 1.8e-39;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||

Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYCCQQRSNWPPFTFGPTKVDIK 108
   |||||
Db 61 RFGSGSGTDFTLTISSLEPEDFAVYCCQQRSNWPPFTFGPTKVDIK 108
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RESULT 15
US-11-021-715-101
; Sequence 101, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-101
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Query Match          94.2%; Score 535; DB 6; Length 108;
Best Local Similarity 94.4%; Pred. No. 2.2e-39;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
   |||||

Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYCCQQRSNWPPFTFGPTKVDIK 108
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Db 61 RFGSGSGTDFTLTISSLEPEDFAVYCCQQRSNWPPFTFGPTKVDIK 108
   |||||
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Job time : 104.462 secs

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OM protein - protein search, using sw model

Run on: December 28, 2005, 14:04:11 ; Search time 6.92308 Seconds  
(without alignments)  
116.825 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPPTFGPGTKVDIK 108

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	94.9	108	7	US-11-093-274-23
2	531.5	93.6	129	6	US-10-721-763-19
3	530.5	93.4	107	7	US-11-093-274-24
4	529	93.1	251	7	US-11-054-515-1049
5	528	93.0	108	7	US-11-093-274-22
6	522.5	92.0	128	6	US-10-721-763-31
7	520.5	91.6	129	6	US-10-721-763-23
8	487.5	85.8	107	7	US-11-040-159-17
9	487	85.7	95	7	US-11-054-669-86
10	487	85.7	95	7	US-11-084-554-138
11	480	84.5	94	7	US-11-093-274-33
12	471	82.9	95	7	US-11-054-669-87
13	471	82.9	95	7	US-11-084-554-131
14	463.5	81.6	131	6	US-10-721-763-27
15	463	81.5	307	7	US-11-000-463-332
16	463	81.5	312	7	US-11-000-463-334
17	462	81.3	251	7	US-11-054-515-1238
18	460	81.0	384	7	US-11-000-463-804
19	460	81.0	384	7	US-11-000-463-805
20	460	81.0	384	7	US-11-000-463-806
21	460	81.0	384	7	US-11-000-463-807
22	459	80.8	247	7	US-11-056-825-8
23	459	80.8	249	7	US-11-056-825-4
24	457.5	80.5	246	7	US-11-054-515-1268
25	456.5	80.4	250	7	US-11-054-515-1952

26	449.5	79.1	246	7	US-11-054-515-1264	Sequence 1264, Ap
27	447.5	78.8	251	7	US-11-054-515-1219	Sequence 1219, Ap
28	447	78.7	253	7	US-11-054-515-1499	Sequence 1499, Ap
29	445	78.3	108	7	US-11-064-174-178	Sequence 178, App
30	444	78.2	106	7	US-11-174-186-7	Sequence 7, Appli
31	441.5	77.7	252	7	US-11-054-515-1534	Sequence 1534, Ap
32	439.5	77.4	254	7	US-11-054-515-905	Sequence 905, App
33	435	76.6	95	7	US-11-054-669-84	Sequence 84, Appl
34	435	76.6	95	7	US-11-054-669-85	Sequence 85, Appl
35	435	76.6	95	7	US-11-084-554-127	Sequence 127, App
36	435	76.6	95	7	US-11-084-554-130	Sequence 130, App
37	434	76.4	108	7	US-11-064-174-177	Sequence 177, App
38	433	76.2	249	7	US-11-054-515-1035	Sequence 1035, Ap
39	432	76.1	213	7	US-11-173-320-4	Sequence 4, Appli
40	432	76.1	213	7	US-11-173-320-4	Sequence 4, Appli
41	429.5	75.6	96	7	US-11-054-669-88	Sequence 88, Appl
42	429.5	75.6	96	7	US-11-084-554-135	Sequence 135, App
43	428	75.4	108	7	US-11-064-174-31	Sequence 31, Appl
44	428	75.4	108	7	US-11-064-174-161	Sequence 161, App
45	425.5	74.9	242	7	US-11-054-515-1844	Sequence 1844, Ap

#### ALIGNMENTS

RESULT 1  
US-11-093-274-23  
; Sequence 23, Application US/11093274  
; Publication No. US2005026608A1  
; GENERAL INFORMATION:  
; APPLICANT: Graziano, Robert  
; APPLICANT: Cardarelli, Josephine M.  
; APPLICANT: Kempe, Thomas  
; APPLICANT: Cutter, Beth  
; APPLICANT: Srinivasan, Mohan  
; TITLE OR INVENTION: IFTA-5 ANTIBODIES AND THEIR USES  
; FILE REFERENCE: 04280/1201101-US1  
; CURRENT APPLICATION NUMBER: US/11/093,274  
; CURRENT FILING DATE: 2005-03-28  
; PRIOR APPLICATION NUMBER: 60/557,741  
; PRIOR FILING DATE: 2004-03-29  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-093-274-23

Query Match 94.9%; Score 539; DB 7; Length 108;  
Best Local Similarity 95.4%; Pred. No. 4.6e-35;  
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	1	EIVLTQSPATLSLSPGERATLS	CRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA	60
Db	1	EIVLTQSPATLSLSPGERATLS	CRASQSVSYLAWYQOKPGQAPRLIYDASNRATGIPA	60
Qy	61	RFGSGSGTDTLTITSSLEPEDFAVYQCQRNWPPTFGPGTKVDIK	108	
Db	61	RFGSGSGTDTLTITSSLEPEDFAVYQCQRNWPPTFGPGTKVDIK	108	

RESULT 2  
US-10-721-763-19  
; Sequence 19, Application US/10721763  
; Publication No. US20050249729A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY  
; FILE REFERENCE: PH-1573-PCT  
; CURRENT APPLICATION NUMBER: US/10/721,763  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: JP2001-150213

```
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match          93.6%; Score 531.5; DB 6; Length 129;
Best Local Similarity 96.3%; Pred. No. 1.9e-34;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNW-PLTFGPGTKVDIK 127

RESULT 3
US-11-093-274-24
; Sequence 24, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-24

Query Match          93.4%; Score 530.5; DB 7; Length 107;
Best Local Similarity 96.3%; Pred. No. 2e-34;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPP-FTFGQTKVKEIK 107

RESULT 4
US-11-054-515-1049
; Sequence 1049, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Euben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1049

Query Match          93.1%; Score 529; DB 7; Length 251;
Best Local Similarity 95.4%; Pred. No. 5e-34;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 143 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 202

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 203 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFLTFGGTKVKEIK 250

RESULT 5
US-11-093-274-22
; Sequence 22, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-22

Query Match          93.0%; Score 528; DB 7; Length 108;
Best Local Similarity 92.6%; Pred. No. 3.1e-34;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQKPGQAPRLIIYDASNRATGIPA 60
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Qy 61 RFGSGSGTDTLTITSSLEPEDFAVYCCQORSNNPPTFGPGTKVDIK 108  
Db 61 RFGSGSGTDTLTITSSLEPEDFAVYCCQQLNNPPTFGPGTKLEIK 108

## RESULT 6

US-10-721-763-31  
; Sequence 31, Application US/10721763  
; Publication No. US20050249729A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; TITLE OF INVENTION: ANTI TRAIL-R ANTI BODY  
; FILE REFERENCE: PH-1573-PCT  
; CURRENT APPLICATION NUMBER: US/10/721,763  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: JP2001-150213  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: JP2001-243040  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: JP2001-314489  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-763-31

Query Match 92.0%; Score 522.5; DB 6; Length 128;  
Best Local Similarity 95.4%; Pred. No. 9.1e-34;  
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFGSGSGTDTLTITSSLEPEDFAVYCCQORSNNPPTFGPGTKVDIK 108  
Db 81 RFGSGSGTDTLTITSSLEPEDFAVYCCQORSNN-PLTFGGGTKVKEIK 127

## RESULT 7

US-10-721-763-23  
; Sequence 23, Application US/10721763  
; Publication No. US20050249729A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; TITLE OF INVENTION: ANTI TRAIL-R ANTI BODY  
; FILE REFERENCE: PH-1573-PCT  
; CURRENT APPLICATION NUMBER: US/10/721,763  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: JP2001-150213  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: JP2001-243040  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: JP2001-314489  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-763-23

Query Match 91.6%; Score 520.5; DB 6; Length 129;  
Best Local Similarity 94.4%; Pred. No. 1.3e-33;  
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGSPA 80

Qy 61 RFGSGSGTDTLTITSSLEPEDFAVYCCQORSNNPPTFGPGTKVDIK 108  
Db 81 RFGSGSGTDTLTITSSLEPEDFAVYCCQORSNW-PLTFGGGTKVDIK 127

## RESULT 8

US-11-040-159-17  
; Sequence 17, Application US/11040159  
; Publication No. US2005025552A1  
; GENERAL INFORMATION:  
; APPLICANT: Flynn, Peter  
; APPLICANT: Luehrs, Kenneth  
; APPLICANT: Balint, Robert F.  
; APPLICANT: Her, Jeng-Hong  
; APPLICANT: Bebbington, Christopher R.  
; APPLICANT: Yarranton, Geoffrey T.  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential  
; FILE REFERENCE: 021167-001730US  
; CURRENT APPLICATION NUMBER: US/11/040,159  
; CURRENT FILING DATE: 2005-01-20  
; PRIOR APPLICATION NUMBER: US 60/537,364  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/546,216  
; PRIOR FILING DATE: 2004-02-23  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: V-region of  
; OTHER INFORMATION: anti-PcrV antibody 1F1 VL  
US-11-040-159-17

Query Match 85.8%; Score 487.5; DB 7; Length 107;  
Best Local Similarity 89.9%; Pred. No. 3.4e-31;  
Matches 98; Conservative 3; Mismatches 5; Indels 3; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTLTITSSLEPEDFAVYCCQORSNN-PPPTFGPGTKVDIK 108  
Db 61 RFGSGSGTDTLTITSSLEPEDFAVYCCQH--FWSTPTVFGGTTKLEIK 107

## RESULT 9

US-11-054-669-86  
; Sequence 86, Application US/11054669  
; Publication No. US20050261480A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
; FILE REFERENCE: 30219/US/3  
; CURRENT APPLICATION NUMBER: US/11/054,669  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: US 10/194,975  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: Patent In version 3.3  
; SEQ ID NO 86  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-669-86

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Query Match      85.7%; Score 487; DB 7; Length 95;
Best Local Similarity 98.9%; Pred. No. 3.4e-31;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
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Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
      |||

QY      61 RFSGSGGTDTFTLTISLLEPEDFAVYYCQQRNWP 95
      |||
Db      61 RFSGSGGTDTFTLTISLLEPEDFAVYYCQQRNWP 95
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RESULT 10
US-11-084-554-138
; Sequence 138, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korvet, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: AEGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-138

Query Match      85.7%; Score 487; DB 7; Length 95;
Best Local Similarity 98.9%; Pred. No. 3.4e-31;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
      |||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
      |||

QY      61 RFSGSGGTDTFTLTISLLEPEDFAVYYCQQRNWP 95
      |||
Db      61 RFSGSGGTDTFTLTISLLEPEDFAVYYCQQRNWP 95
      |||

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November 2005

Published\_Applications\_Nucleic Acid and Published\_Applications\_Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_NA\_Main) and **.rapbn** (Published\_Applications\_NA\_New).  
Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2005, 14:04:11 ; Search time 8.07692 Seconds  
(without alignments)  
116.825 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QVQLVESGGGVQPGRSRLR.....NYYYGMDVWGQGTTVTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

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Database : Published Applications AA_New:
1: /cgn2_6/podata/1/pubpaa/US0
2: /cgn2_6/podata/1/pubpaa/US0
3: /cgn2_6/podata/1/pubpaa/US0
4: /cgn2_6/podata/1/pubpaa/US0
5: /cgn2_6/podata/1/pubpaa/US0
6: /cgn2_6/podata/1/pubpaa/US1
7: /cgn2_6/podata/1/pubpaa/US1
8: /cgn2_6/podata/1/pubpaa/US6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	572.5	85.7	252	7	US-11-054-515-1731	Sequence 1731, Ap
2	565	84.6	126	7	US-11-064-174-26	Sequence 26, Appl
3	560	83.8	249	7	US-11-054-515-512	Sequence 512, App
4	559	83.7	126	7	US-11-064-174-153	Sequence 153, App
5	557	83.4	126	7	US-11-064-174-25	Sequence 25, Appl
6	554	82.9	247	7	US-11-054-515-1330	Sequence 1330, Ap
7	554	82.9	256	7	US-11-054-515-839	Sequence 839, App
8	550.5	82.4	252	7	US-11-054-515-1394	Sequence 1394, Ap
9	549	82.2	254	7	US-11-054-515-981	Sequence 981, App
10	548.5	82.1	125	7	US-11-064-174-140	Sequence 140, App
11	547.5	82.0	125	7	US-11-084-554-8	Sequence 8, Appli
12	546	81.7	249	7	US-11-054-515-397	Sequence 397, App
13	546	81.7	249	7	US-11-054-515-1102	Sequence 1102, Ap
14	546	81.7	249	7	US-11-054-515-1115	Sequence 1115, Ap
15	545	81.6	249	7	US-11-054-515-1724	Sequence 1724, Ap
16	545	81.6	249	7	US-11-054-515-1725	Sequence 1725, Ap
17	544	81.4	124	7	US-11-040-159-14	Sequence 14, Appl
18	544	81.4	249	7	US-11-054-515-911	Sequence 911, App
19	544	81.4	249	7	US-11-054-515-1113	Sequence 1113, Ap
20	543	81.3	249	7	US-11-054-515-1119	Sequence 1119, Ap
21	543	81.3	252	7	US-11-054-515-1627	Sequence 1627, Ap
22	542	81.1	249	7	US-11-054-515-1117	Sequence 1117, Ap
23	541	81.0	249	7	US-11-054-515-1118	Sequence 1118, Ap
24	539	80.7	247	7	US-11-054-515-924	Sequence 924, App
25	539	80.7	247	7	US-11-054-515-892	Sequence 892, App

Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRLLEYDILT-GYIIYYGMDVW 119  
 QY 117 QGTTVTVSS 126  
 Db 120 GRGTLVTVSS 129

RESULT 2

US-11-064-174-26  
 ; Sequence 26, Application US/11064174  
 ; Publication No. US20050282252A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siegel, Donald L.  
 ; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
 ; FILE REFERENCE: 09596-42U2  
 ; CURRENT APPLICATION NUMBER: US/11/064,174  
 ; CURRENT FILING DATE: 2005-02-22  
 ; PRIOR APPLICATION NUMBER: US/09/240,274  
 ; PRIOR FILING DATE: 1999-01-29  
 ; PRIOR\*APPLICATION NUMBER: 60/081,380  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: 60/028,550  
 ; PRIOR FILING DATE: 1996-10-11  
 ; NUMBER OF SEQ ID NOS: 224  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 26  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: anti-Rh(D) chain D31  
 US-11-064-174-26

Query Match 84.6%; Score 565; DB 7; Length 126;  
 Best Local Similarity 84.1%; Pred. No. 1.2e-41;  
 Matches 106; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
 Db 1 EVQLLESQGGVQPGSRSLRLSCAASGFTFSSYGMHWVRQAPGKGLWVAVVYDGSNKHY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRGTAAAGNYYIYGMVWGQGT 120  
 Db 61 SDSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARERNFRSGYSRYIYGMVWGPGT 120  
 QY 121 TVTVSS 126  
 Db 121 TVTVSS 126

RESULT 3

US-11-054-515-512  
 ; Sequence 512, Application US/11054515  
 ; Publication No. US2005025532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
 ; FILE REFERENCE: PF523P3  
 ; CURRENT APPLICATION NUMBER: US/11/054,515  
 ; CURRENT FILING DATE: 2005-02-10  
 ; PRIOR APPLICATION NUMBER: 60/543,296  
 ; PRIOR FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: 60/580,347  
 ; PRIOR FILING DATE: 2004-06-18  
 ; PRIOR APPLICATION NUMBER: 10/293,418  
 ; PRIOR FILING DATE: 2002-11-14  
 ; PRIOR APPLICATION NUMBER: 60/331,469  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 60/340,817  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 09/880,748  
 ; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 3247  
 ; SEQ ID NO 512  
 ; LENGTH: 249  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-054-515-512

Query Match 83.8%; Score 560; DB 7; Length 249;  
 Best Local Similarity 86.5%; Pred. No. 6.1e-41;  
 Matches 109; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
 Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSSYGMHWVRQAPGKGLWVAVVYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRGTAAAGNYYIYGMVWGQGT 120  
 Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDGYDILTGYIYGMVWGQGT 120  
 QY 121 TVTVSS 126  
 Db 121 MVTVSS 126

RESULT 4

US-11-064-174-153  
 ; Sequence 153, Application US/11064174  
 ; Publication No. US20050282252A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siegel, Donald L.  
 ; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
 ; FILE REFERENCE: 09596-42U2  
 ; CURRENT APPLICATION NUMBER: US/11/064,174  
 ; CURRENT FILING DATE: 2005-02-22  
 ; PRIOR APPLICATION NUMBER: US/09/240,274  
 ; PRIOR FILING DATE: 1999-01-29  
 ; PRIOR APPLICATION NUMBER: 60/081,380  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: 60/028,550  
 ; PRIOR FILING DATE: 1996-10-11  
 ; NUMBER OF SEQ ID NOS: 224  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 153  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH56  
 US-11-064-174-153

Query Match 83.7%; Score 559; DB 7; Length 126;  
 Best Local Similarity 83.3%; Pred. No. 4e-41;  
 Matches 105; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
 Db 1 EVQLLESQGGVQPGSRSLRLSCAASGFTFSSYGMHWVRQAPGKGLWVAVVYDGSNKHY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRGTAAAGNYYIYGMVWGQGT 120  
 Db 61 SDSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARERNFRSGYSRYIYGMVWGPGT 120  
 QY 121 TVTVSS 126



КУЧА 61



```
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-11-084-174-140

Query Match      82.1%; Score 548.5; DB 7; Length 125;
Best Local Similarity 83.3%; Pred. No. 3e-40;
Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRSLRLSCAASGTFPSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGVQPGSRSLRLSCAASGTFPSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGIAAGNYYTGMVWGQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDQOR-AAAGIFYYSRMDVWGQGT 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 TTVTVSS 126
   :|||:|||||
Db 120 TTVTVSS 125

RESULT 11
US-11-084-554-8
; Sequence 8, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-8

Query Match      82.0%; Score 547.5; DB 7; Length 125;
Best Local Similarity 86.5%; Pred. No. 3.6e-40;
Matches 109; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRSLRLSCAASGTFPSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGGVQPGSRSLRLSCAASGTFPSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGIAAGNYYTGMVWGQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAREVSAMGG-PYINGMDVWGQGT 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 TTVTVSS 126
   :|||:|||||
Db 120 TTVTVSS 125

RESULT 12
US-11-054-515-397
; Sequence 397, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
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; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1102
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1102

Query Match      81.7%; Score 546; DB 7; Length 249;
Best Local Similarity 84.1%; Pred. No. 9.2e-40;
Matches 106; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSVYAMHWVRQAPGNGLEWVAFPMYSYDGSNKYY 60
Db 1 EVNLRSGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYTGYGMDVWGQGT 120
Db 1 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYTGYGMDVWGQGT 120

Qy 121 TVTVSS 126
Db 121 MVTVSS 126

RESULT 14
US-11-054-515-1115
; Sequence 1115, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1115
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1115

Query Match      81.7%; Score 546; DB 7; Length 249;
Best Local Similarity 84.1%; Pred. No. 9.2e-40;
Matches 106; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSVYAMHWVRQAPGNGLEWVAFPMYSYDGSNKYY 60
Db 1 EVNLRSGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYTGYGMDVWGQGT 120
Db 1 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYTGYGMDVWGQGT 120

Qy 121 TVTVSS 126
Db 121 MVTVSS 126

RESULT 15
US-11-054-515-1724
; Sequence 1724, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1724
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1724

Query Match      81.6%; Score 545; DB 7; Length 249;
Best Local Similarity 84.1%; Pred. No. 1.1e-39;
Matches 106; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSVYAMHWVRQAPGNGLEWVAFPMYSYDGSNKYY 60
Db 1 QVNLRSGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYTGYGMDVWGQGT 120
Db 1 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYTGYGMDVWGQGT 120

Qy 121 TVTVSS 126
Db 121 MVTVSS 126

Search completed: December 28, 2005, 14:23:17
Job time : 9.07692 secs
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# WEST Search History

Hide Items

Restore

Clear

Cancel

DATE: Friday, January 06, 2006

Hide? Set Name Query Hit Count

DB=USPT; PLUR=YES; OP=OR

<input type="checkbox"/>	L2	L1 with human	41
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<input type="checkbox"/>	L1	anti adj Tnf adj antibody	338
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END OF SEARCH HISTORY

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STIC-Biotech/ChemLib

175117

From: Seharaseyon, Jegatheesan  
Sent: Tuesday, December 27, 2005 3:25 PM  
To: STIC-Biotech/ChemLib  
Subject: Re:09/920137

Importance: High

Hi,

Please search SEQ ID NO: 7 and 8 of 09/920137 in both the commercial and interference databases.

Thanks in advance,  
Seyon.

J. Seharaseyon  
Art Unit 1647  
Remsen 4C61  
Mailbox 4C70  
Phone: (571)-272-0892  
Fax: (571)-273-0892

VRF E

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

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Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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